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RESULT 1
AX107722
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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1 Donoho,G., Turner,C.A., Nehls,M., Friedrich,G., Zambrowicz, Sands,A.T. Human kinase proteins and polynucleotides encoding the same

Craniata; Vertebrata; Euteleostomi Catarrhini; Hominidae; Homo.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz
Sands, A.T.
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Patent: WO 0123579-A 5 05-APR-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers

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Patent: WO 0179488-A 3 25-OCT-2001
Millennium Pharmaceuticals, Inc. ()
Location/Qualifiers
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/organism="Homo sapiens"
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Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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LOCUS LOCUS LOCUS AXOS6404 DII bp DNA linear PAT 13-JAN-2001 DEFINITION Sequence 48 from Patent W00073469. ACCESSION AXOS6404. AXOS6404.i GI:12291:1 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) REFERENCE LOCATION Mammalia; Eutheria; Primates; Catarrhini; Hominidac; Homo. REFERENCE AUTHORS Plowman, G.D., Martinez, R., Whyte, D. and Sudersanam, S. TITLE Protein Kinases JOURNAL SOURCE JOURNAL Patent: WC 0033469-A 48 07-DEC-200; Sugen, Inc. (US) FEATURES i. 911 /organism="Homo sapiens" /db_xref="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 293 a 182 c 178 g 258 t ORIGIN	Query Match Best Local Similarity 100.0%; Pred. No. 1.1e-136; Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 285 AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA 344 	Qy 	Qy 405 TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA 464 	Qy 465 TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGA 524	Qy 525 TACTCAGTATGGTTCTTCAGTCGATATATGGCTATTGGTTGTGTTTTTGCAGAGCTCCT 584 	Oy 585 GACAGGCCACTGTGGCCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAG 644 [Qy 645 AACACTAGGAAATTAATCCCAAGACATCAATCTTTAAAGTAACGGGTTTTTCCA 704 	Oy 705 TGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAGTTCTCAGATGT 764 	Oy 765 TCATCCTGTGGCTCTGAACTTCATGAAGGGTGTCTGAAGATGAATCCAGATGACGAAT 824 	Oy 825 AACCTGTTCCCAACTCCTGGAGGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAA 884 	Qy 885 AAGAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAG 927 \	RESULT 10 AX056405

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Lexicon Genetics Incorporated (US)
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Patent: WO 0218424-A 146 07-MAR-2002;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

I (bases 1 to 1363)

Meyerson, M.; Enders, G.H., Wu, C.L., Su, L.K., Gorka, C., Ne

Harlow, E. and Tsai, L.H.

A family of human cdc2-related protein kinases

EMBO J. 11 (8), 2909-2917 (1992)

92347325

1639063

2 (bases 1 to 1363)

Meyerson, M.L.

Direct Submission

Submitted (12-MAY-1992) M.L. Meyerson, Massachusetts Gen

Hospital, Cancer Center, Bldg 149, 13th Street, Charlest

02129, USA
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ALIGNMENTS

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Location/Qualifiers
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/*tag= a
/product= "Human kinase #6"
/note= "The coding region does not include stop codon"
/partial
                                                                         Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder; ss.
                 E)
               AAD03817 standard; cDNA; 945
                                                                                                                                                                                                                                     (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                      2000WO-US26621.
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                                              (first entry)
                                                            Human kinase cDNA #6
                                                                                                                                                                       WO200123579-A1
                                                                                                   Homo sapiens
                                                                                                                                                                                                      27-SEP-2000;
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                                             19-JUN-2001
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                              AAD03817;
RESULT 1
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The present sequence is a cDNA encoding novel human protein

(NHP) known as human kinase. The human kinases share structural

similarity with animal kinases, more particularly serine or

threonine protein kinases. Human kinase cDNA is useful for the

detection of mutant human kinase for the diagnosis of disease,

and also as a therapeutic. It is useful for screening drugs

effective in the treatment of symptomatic or phenotypic

manifestations perturbing the normal function of NHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

chiantification of other cellular gene products related to human

kinases, and as reagents in assays for screening compounds that

are useful for treating mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics are used to genetically engineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

encoding functional NHPs are used in gene therapy for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseasements.
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Pred. No. 4e-3
0; Mismatches
            Friedrich
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P-PSDB; AAE00495.
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Best Local Similarity
Matches 945; Conser
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/note= "The coding region does not include
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biological disorder; ss.
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P-PSDB; AAE00492.
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11-AUG-2000;
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                                  The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the antibodies, as reagents in diagnostic assays, for the kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonuclectides are used as probes. The labelled NHP probes are used in diagnostics and pharmacogenomics. Nucleotide construct be used in diagnostics and pharmacogenomics. Nucleotide constructs in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression.
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Mismatches 0; Indels
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biological
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treating mental,
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useful for
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Best Local Similarity
Matches 929; Conser
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compounds
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GAGCCAGAAGACATGGAAACTCTTGAGGAAAGTTCTCAGATGTTCATCCTGTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGAGGAAAGTTCTCAGATGTTCATCCTGTGGCTCTGGCTCTGAGGAAAGTTCTCAGATGTTCATCTGAGGAAAGTTCTCAGATGTTCATCTGAGGAAAAGTTCTCAGATGTTCTTGAGGAAAAGTTCTCAGATGTTCATCTGAGGAAAAGTTCTAAAGTTCTAATCCTGTGGCTCTG
                                                                                                                                                                                                                                                                                                                           AACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC
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239..1267
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The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's cyndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, of Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of drug screening techniques and to analyse the proteome of a bissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. PKIN is useful in southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (EDISA)-like assays and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PKIN-10 cDNA.
                                                                                                         kinase polypeptide, useful in diagnosis, prevention of cancer, immune disorder, growth and developmental cardiovascular disorder and lipid disorder -
                                                                                                                                                                                                                  Claim 5; Page 183; 196pp; English
                            WPI; 2002-206083/26
P-PSDB; AAE19152.
                                                                                                             New human
                                                                                                                                       treatment
disorder,
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Sequence 1790 BP; 581 A; 328 C; 366 G; 515 T; 0 other;

Gaps .. 0 Length 1790; Indels Score 927; DB 24; I Pred. No. 3.7e-240; ., С Wismatches 98.1%; SCC 100.0%; Pr Conservative Query Match Best Local Similarity Matches 927; Conserv ે

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GAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGAGGAAAGTTCTCAGATGTTCATCTCTGTGGCTCTGTGGCTCTGAGGAAAGTTCTCAGATGTTCATCTCTGAGGAAAAGTTCTCAGATGATCATCTGAGGAAAAGTTCTCAGATGTTCATGAGGAAAAGTTCTCAGATGATCATCATGAGCTCTG AACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCAACTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGATGAAGAGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAAGTC TGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCCAAATTAAAAGAAAAGCACGTAAT ATCCCAAGACATCAATCATTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 927 Ú 721 019 106 661 781 079 841 σ, 60 83 83 95 a qq d ò õ ò 음 ਨੇ

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9 # protein 1678 DITHP entry CDNA; human (first standard; encoding 21-JAN-2003 ABX08936 ABX08936 CENA RESULT 4 ABX08936

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Human; ss; gene; diagnostic and therapeutic; DITHP; cancer; arteriosclerosis atherosclerosis; psoriasis; primary thrombocytopenia; autoimmune; inflammatory; anaemia; asthma; autoimmune thyroiditis; crohn; s disease; diabetes mellitus; glomerulonephritis; gout; stroke; multiple sclerosis; rheumatoid arthritis; uveitis; AIDS; allergy; acquired immunodeficiency disease; neurological disorder; epilepsy; Alzheimer's disease; dementia; mental retardation; gastrointestinal; Parkinson's disease; ulcer; cirrhosis; reproductive; infertility; endometriosis; endocrine disorder; hyperparathyroidism; hyperlipidemia; hypercholesterolaemia; hypoglycaemia; obesity; Reiter's syndrome; connective tissue disorder; osteoporosis; infection.

sapiens Homo WO200279473-A2 10-0CT-2002

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2001US-261652P. 2001US-261864P. 2001US-262164P. 2001US-262207P. 2001US-262209P. 2001US-262209P. 2001US-262209P. 2001US-26215P. 2001US-263102P. 2001US-263063P. 2001US-263063P. 2002WO-US01009 12-JAN-2001; 16-JAN-2001; 16-JAN-2001; 17-JAN-2001; 17-JAN-2001; 17-JAN-2001; 17-JAN-2001; 19-JAN-2001; 19-JAN-2001; 09-JAN-2002;

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Pred. No. 1.9
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Gerstin EH, Peralta CH,
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Best Local Similarity 99.2%;
Matches 925; Conservative
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P-PSDB; ABU05290.
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                                                                                             ATGTAGCTA-CGAGATGGTACCGAGCT-CCTGAACTTCTTGTGGGAGATACT-CAGTATG
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Claim 1; Page 31-32; 38pp; English
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biological disorder, ss.
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                                                                               AASO6701-AASO6757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides cor serine/threonine kinase (PTK and STK) families. The polynucleotides protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disease (e.g. schizophrenia), neurodegenerative disorders (e.g. disease), inflammatory disorders (e.g. infertility).

Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays.

The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.
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Pred. No. 5.9e-223;
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Best Local Similarity 94.5%;
Matches 927; Conservative
                                                                   Example 1; Figure 1;
         WPI; 2001-343950/36
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                                                                                                                                                                   New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical disease
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The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the antibodies, as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are used as probes. The labelled hat can be useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide constructs encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the
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Pred. No. 1.8e-216;
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The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kirases share structural similarity with animal kinases, more particularly serine or threonine protein kinases, Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the intendication of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are used as probes. The labelled MHP products are used as probes. The labelled construct constitutions within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide constructs in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs endulation of NHP in the body. Nucleotide constructs
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Pred. No. 3.8e-212;
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ilarity 90.6%;
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Best Local Similarity
Matches 929; Conser
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1020 650 744 840 804 006 924 sorder; AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive; antiinflammatory; antithyroid; antipsoriatic; cphthalmological; antiallergic; antiasthmatic; antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide; anorectic; metabolic; immunomodulator; analgesic; cellular proliferative disorder; acute lymphoblastic leukaemia; Hodgkin's disease; bone metabolism disorder; osteoporosis; immune system disorder; inflammatory; diabetes mellitus; osteoarthritis; asthma; cardiovascular disorder; hypertension; coronary artery disease; endothelial cell disorder; psoriasis; ss. "Protein kinase Location/Qualifiers
1..128
/*tag= a
129..815
/*tag= b
/product= "Protein ki
816..882
/*tag= c ណ ប 882 (MILL-) MILLENNIUM PHARM INC 2000US-196910P 2001WO-US12188 entry) CDNA; CDNA (first standard; 14257 929 102 CAGGT CAGGI WO200179488-A2 13-APR-2000; Humar kinase 3-APR-2001; sapiens 08-MAR-2002 25-OCT-2001 LT 8 1248 AAI64248 AAI64248; 1021 781 94. 802 901 685 745 865 961 S 661 651 651 Key 5'UTR 3'UTR HOLLO 검 a $\overset{\circ}{\sigma}$ 55 d ઠે qq ò ò δ ਨੇ

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The invention relates to an isolated 14257 polypeptide and nucleic acid encoding it. The 14257 protein is a protein kinase that acts as a modulating agent in regulating a variety of cellular processes, including cell proliferation, differentiation, growth and division. The activity of the protein of the invention may be described as; cytostatic; osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive, antinilammatory; antiarthyroid; antiatherosclerotic; hypotensive; vasotropic; antiarthythmic; virucide; anorectic; metabolic; immunomodulator and analgesic. The protein of the invention may act as a novel diagnostic target or therapeutic agent controlling certain disorders, for example kinase-associated or other 14257-associated disorders uch as cancers e.g. acute lymphoblastic leukemia or Hodgkin's disorders such as cancers include bone metabolism disorders such as osteoporosis, disorders of the immune system, e.g. inflammatory, diabetes mellitus, osteoarthritis and asthma. Proteins of the invention may also be of use as therapeutic agents in cardiovascular disorders such as hypertension and coronary artery disease, and some endothelial cell disorders, including psoriasis. The current sequence represents a human kinase 14257 cDNA.
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                                                                   New 14257 polypeptides (protein kinases), useful as diagnostic and therapeutic agents for controlling cellular proliferative differentiative disorder, bone disorders, immune disorders and cardiovascular disorders -
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Pred. No. 3.3e-164;
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Matches 649; Conservative
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B; AAG78547.
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The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase expression and activity. Diseases related to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, cardiomyopathies, strokes, renal failure, immune disorders cardiomyopathies, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders. 668 909 728 acids encoding kinase polypeptides, useful for diagnosing and jimune-related diseases and disorders, cardiovascular disease yenerative diseases and/or cancers -Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopath: immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune discrder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss. 655 T; 0 other; S Sudersanam G; 258 **4** SEQ ID NO: C; 178 à English ВР Whyte 911 A; 182 2000WO-US14842 99US-0136503 Novel protein kinase cDNA, entry) 310pp; CDNA; ď Martinez 293 (first WPI; 2001-032161/04 P-PSDB; AAB65642. standard; HNC. 5: neurodegenerative 8P; 4; F19 WO200073469-A2 SUGEN 911 26-MAY-2000; Homo sapiens 8-MAY-1999; 07-DEC-2000 g, 27-MAR-2301 AAF44669; AAF44669 treating 699 Seguence 609 541 109 729 (SUGE-) Plowman Nucleic Example RESULT AAF4466 g õ ò

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The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase antibodies antibodies antibodies of kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, cardiomyopathies, strokes, renal failure, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.
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Hillman JL, Yu JY, Tuason C, Yap PE, Amshey SR;
I, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gersti
David MH, Lewis SA, Chen AJ, Panzer SR, Harris
Aarwaha R, Lo A, Lan RY, Urashka ME;
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2001US-280067P.
2001US-291280P.
2001US-291829P.
2001US-291849P.
2001US-299428P.
2001US-299428P.
2001US-299428P.
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16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
20-JUN-2001;
20-JUN-2001;
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Dufour GE,
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, costeopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are protein replacement therapy and are useful for treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, including adenocarcinoma, including including adenocarcinoma, including including adenocarcinoma, selectiones, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis, ABX34440-ABX34835 encode the MDDT polypeptides represented in hepatitis, ABX34440-ABX34835 encode the MDDT polypeptides represented in ABUI1450-ABUI1845, described in the disclosure of the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                  Friedrich G,
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"polymorphism site;
                                                                              bioreactor;
                                                                                                                                                                                           "Human kinase
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                                                                                                                                Location/Qualifiers
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/*tag= a
                                                                            Human, kinase, gene therapy, biored biological disorder, polymorphism,
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                                                       Human kinase
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Length 1819;

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AB277126 to AB277165 encode the human protein kinases given in ABP96048 to ABP96087. The protein kinases have antiasthmatic, antinflammatory, antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic, immunosuppressive and vulnerary activities, and can be used in gene therapy. A protein kinase therapeutic agent from the present invention, particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease, migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers (e.g. leukaemias) or wound granulation.
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                                                                                                                                                       Sequence 1086 BP; 356 A; 227 C; 210 G; 293 T; 0 other;
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Pred. No. 3.6e-125;
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Best Local Similarity 100
Matches 501, Conservative
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AC AADO3812;
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DE Human kins
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CS Homo sapie
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CS Homo sapie
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                         CCTGCCGTAGCCTCTCAAAGTGCTGGAATTACAGGAAAATTAATCCCCAAGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarctiallograft rejection or cancers
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/product= "protein kinase"
/note= "no start or stop c
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1..1086
/*tag= a
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2001US-332870P
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P-PSDB; ABP96087.
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06-NOV-2001;
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New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases
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(NHP) known as human kinase. The human kinases share structural

similarity with animal kinases, more particularly serine or

threonine protein kinases. Human kinase cDNA is useful for the

detection of mutant human kinase for the diagnosis of disease,

and also as a therapeutic. It is useful for screening drugs

effective in the treatment of symptomatic or phenotypic

manifestations perturbing the normal function of NHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

chartification of other cellular gene products related to human

kinases, and as reagents in assays for screening compounds that

are useful for treating mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics and pharmacogenomics. Nucleotide construct

encoding NHP products are used to genetically engineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

encoding functional NHPs are used in gene therapy for the

modularion of NHP encodes.
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/*tag= a
/product= "Human kinase #1"
/note= "The coding region does not
/partial
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Pred. No. 1.1e-112;
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ilarity 99.8%;
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P-PSDB; AAE00490.
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Best Local S
Matches 455
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/*tag= a
/product= "Human kinase #4"
/note= "The coding region does not include stop codon"
                                    New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases
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(NHP) known as human kinase. The human kinases share structural
similarity with animal kinases, more particularly serine or
threonine protein kinases. Human kinase cDNA is useful for the
detection of mutant human kinase for the diagnosis of disease,
and also as a therapeutic. It is useful for screening drugs
effective in the treatment of symptomatic or phenotypic
manifestations perturbing the normal function of NHP in the
body. The NHP nucleotide sequences are useful for generation of
antibodies, as reagents in diagnostic assays, for the
identification of other cellular gene products related to human
kinases, and as reagents in assays for screening compounds that
are useful for treating mental, biological or medical disorders.
NHP oligonucleotides are used as probes. The labelled NHP probes
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P-PSDB; AAE00493.
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are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression.
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Sequence 9, Application US/08874347
Parent No. 5863741
GENERAL INFORMATION:
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Thomas, Charles F.
APPLICANT: Thomas, Carles F.
APPLICANT: Thomas, Carles F.
APPLICANT: COST OF COCC PROTEIN KINASE FRO
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 330(CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
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Sequence 3, Application US/09411628

Patent No. 6428994

GENERAL INFORMATION:
APPLICANT: University of Southern California
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: US 6C/102,906
EARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Leof, Edward B.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROTELE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300 CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
                                                                                                                                                                                                                           TCCCAACTCCTGGAGGCTCCTACTTTGATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
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08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874,347
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Windows
                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09093522
Patent No. 6015700
GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Diskette
IBM Compatible
SYSTEM: DOS
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FILING DATE: 08-JU
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SOFTWARE: FastSEC
CURRENT APPLICATION
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Pred. No. 5e-39;
0; Mismatches 4
                              0
                                                    APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                             Sequence
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il Similarity 52.3%;
458; Conservative
Compatible
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nucleic acid
EDNESS: single
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; LOCATION: 1...900
; OTHER INFORMATION:
US-08-874-347-9
                                                                                                                                                                                                                                                                                                TOPOLOGY: 1:
MOLECULE TYPE:
FEATURE:
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NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the A
                                                      ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                         New York
: USA
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Best Local Similarity
                                 New York
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                ADDRESSEE
STREET:
CITY: Ne
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Pred. No. 5e-3
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US-08-969-106-1
; Sequence 1, Application US/0896
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 II
.1 Similarity 52.3%; 458; Conservative
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Pred. No. 1.5e-36;
); Mismatches 291;
                                                                                                                  MEDIUM.
COMPUTER: IBM COMP.
COMPUTER: IBM COMP.
CORFATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEFAX: 212-869-9741
TELEFAX: 212-869-9741
TELEFAX: 56141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION: 1...894
OTHER INFORMATION:
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US-09-266-225D-13
US-09-266-225D-13
Sequence 13, Application US/09266225D
Fatent No. 6573364
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishan
APPLICANT: Kingsmore, Stephen
APPLICANT: Tchernev, Velizar
TITLE OF INVENTION: Isolation and Characterization of Her
TITLE OF INVENTION: Syndrome (HFS) Protein Complexes and
TITLE OF INVENTION: Interacting Proteins
FILE REFERENCE: 15966-523
CURRENT APPLICATION NUMBER: US/09/266,225D
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 1.5e-36;
); Mismatches 291;
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Best Local Similarity 55.1%;
Matches 364; Conservative
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Pred. No. 1.5e-36;
); Mismatches 291;
                                                                                                                                                                                                                                                                                                                                                                                              STALE: New YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC Version 2.0
CURRENT APPLICATION NUMBER: US/09/338,125
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                                                                                                                                                                                                                                                                                                                    CDK2 INTERACTIONS
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
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R: 7934-057
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US-09-338-125-1

Sequence 1, Application US/09338125

Patent No. 6521412

GENERAL INFORMATION:

APPLICANT: Yang, M.

APPLICANT: Schulz, V.

TITLE OF INVENTION: CDK2 INTERACT

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Amer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEFAX: 66141 PENNIE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 bare
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Score 163.4; DB 4;
Pred. No. 1.6e-36;
; Mismatches 291;
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US-09-417-197-114
Sequence 114, Application US/09417197
Patent No. 6518021
GENERAL INFORMATION:
TITLE OF INVENTION: A Method For Extracting Quirelle OF INVENTION: On A Cellular Response FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 114
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EGFP-CDK2 fusion
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Conservative
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                                         GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT
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Quantitative
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; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Qu.; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
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) LOCATION: (1)..(1632)
US-09-417-197-112
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ORGANISM: Artificial
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                                                                                        Score 155.6; DE Pred. No. 2e-34; 0; Mismatches
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US-09-620-312D-313
i Sequence 313, Application US/09620312D
j Patent No. 6569662
j GENERAL INFORMATION:
i APPLICANT: Tang, Y. Tom
j APPLICANT: Liu, Chenghua
j APPLICANT: Asundi, Vinod
j APPLICANT: Zhang, Jie
j APPLICANT: Ren, Feiyan
j APPLICANT: Chen, Rui-hong
j APPLICANT: Zhao, Qing A.
 SEQ ID NOS: 191
FastSEQ for Windows Version
                                                                                          16.5%;
54.4%;
                                                                                                    l Similarity 54. 361; Conservative
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US-09-220-132-3
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NUMBER OF SE
SOFTWARE: F
SEQ ID NO 3
LENGTH: 105
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                                                                                Gaps
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Patent No. 6506607
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND CCMPOSITONS FOR THE IDENTIFICATION
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS
FILE REFERENCE: 07334-074001
                                                                                                                   CCAAATCTTGTGAACCTCATGGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAG
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9-36;
291;
                                                         Score 163.4; DB
Pred. No. 1.6e-3
0; Mismatches 2
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CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
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ilarity 55.1%;
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364; Conser
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    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-09-417-197-114
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Pred. No. 1.8e-28;
); Mismatches 309;
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CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/991,997
FILING DATE: 19-NOV-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/963,308
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1993
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/901,514
FILING DATE: 26-MAY-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1993
ATTORNEY/AGENT INFORMATION:
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E: Floppy disk
IBM PC compatible
TWETTEM: PC-DOS/MS-DOS
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US-08-154-915-1
Sequence 1, Application US/08154915
Patent No. 5618669
GENERAL INFORMATION:
APPLICANT: Beach, David
APPLICANT: Xiong, Yue
TITLE OF INVENTION: Related Theret
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
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TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NC: I:
SEQUENCE CHARACTERISTICS:
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l Similarity 52.3%;
346; Conservative
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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Fred. No. 6.1e-29;
; Mismatches 309;
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                                         APPLICANT: Mang, John Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C122B
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: Pt_genes Version 1.0
SEQ ID NO 313
LENGTH: 1825
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Best Local Similarity 52.5%;
Matches 348; Conservative
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LOCATION: (234)..(1235)
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Best Local Similarity 52.3%; Pred. No. 1.8e-28; Matches 346; Conservative 0; Mismatches 309
FILING DATE: 16-OCT-1992

APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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; LOCATION:
US-08-464-517-37
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/08464517
Sequence 37, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
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60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKE
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MEDIUM TYPE: Floppy disk
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STATE:
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
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US-08-463-772-37
; Sequence 37, Application US/08463772
; Patent No. 6066501
; GENERAL INFORMATION:
; TITLE OF INVENTION: D-TYPE CYCLIN ;
; TITLE OF INVENTION: D-TYPE CYCLIN ;
; TORRESPONDENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSE: LAHIVE & COCKFIELD STREET: 6C State Street
CITY: Boston
; COUNTRY: USA
; ZIP: 02109
; ZIP: 02109
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US/08/463,
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TOMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-;
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: FIOPPY GISK
COMPUTER: IBM PC Compatible
COMPUTER: ASCII(text)
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-WAY-1994
CLASSIFICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 26-WAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-304C
TELECOMMUNICATION INFORMATION:
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S-08-246-361A-37
Sequence 37, Application US/08246361A
Sequence 37, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN A
ITTLE OF INVENTION: D-TYPE CYCLIN A
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
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     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
TELECOMMUNICATION INFORMATION:
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CE 1 (bases 1 to 695)
RS Adelson, D.L. and Gill, C.A.
Contact: David L. Adelson
Animal Breeding and Genetics
Texas ALM University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798456970
Email: david.adelson@tamu.edu.
Email: david.adelson@tamu.edu.
Bmail: david.adelson@tamu.edu.
Location/Qualifiers
II. 695
/organism="Bos taurus"
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AV0661797
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kond: Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyo:
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Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,

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Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,

Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,

Yoshino,M., Muramatsu,M. and Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Submitted, Japan (B-mail-genome-rese@gsc.riken.go.jp/, Tel:81-45-503-9222,

RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail-genome-rese@gsc.riken.go.jp/, Tel:81-45-503-9222,

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cDNA library was prepared and sequenced in Mouse Genome

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues. First strand cDNA was primed with a primer

[5' GAGAGAGAGCATCCTTTTTTTTTTTTTTTVN 3'], cDNA was
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Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933411017 product:cyclin-dependent kinase-like 1 (CDC2-related kinase), full insert sequence.

AKO16781

AKO16781.

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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I Similarity 66.9%; Pred. No. 2e-78;
587; Conservative 0; Mismatches 287;
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sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
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S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: John C. Marshall, M.D., Ph.D

CDNA Library Preparation: CLONTECH

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM3144 row: i column: 16

High quality sequence stop: 468.

Location/Qualifiers

Location/Qualifiers

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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AGENCOURT 11526413 NICHD Rr Pit1 Rattus IMAGE:6888377 5', mRNA sequence.
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CB315094.1 GI:28838974
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(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

188 c 200 g 202 t i others
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos'
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos'
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 536)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gdiscovery
Genome Res. 6 (9), 791-806 (1996)
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8889548
Contact: McCray, PB
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UI-CF-DU1-adn-i-10-0-UI.sl UI-CF-DU1 Homo sapiens UI-CF-DU1-adn-i-10-0-UI 3', mRNA sequence.
BU686325
BU686325.1 GI:23541120
EST.
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                                                                                Score 390.6; DB 14;
Pred. No. 5.2e-76;
); Mismatches 90;
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il Similarity 83.3%;
455; Conservative
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Location/Qualifiers

1. 536
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University of Icwa
2024 University of Icwa Med Labs, Iowa City, IA 52242, USA
2024 University of Icwa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Icwa
CDNA Library preparation: Dr. M. Bento Soares, University of Icwa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Icwa
DNA Sequencing by: Dr. M. Bento Soares, University of Icwa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
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Pred. No. 1.7e-69;
0; Mismatches 0;
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100.0%; Pri
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SM Mus muscilla; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1 (bases 1 to 689).

Si (bases 1 to 68).

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagatik., Teuruno, M., Hasegawa, Y., Nogami, A., Schombach, C., Golobori, T., Baldarefli, R., Hill, D.P., Bult, C., Hume, D.A., Golobori, T., Baldarefli, R., Hill, D.P., Bult, C., Hume, D.A., Batalow, S., Charlin, C., Chothai, C., Cousins, S., Dalla, E., Dragami, T., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M. Gissi, C., Godzik, A., A., Frazer, K.S., Gasterland, T., Cariboldi, M., Gissi, C., Godzik, R., M., Frazer, K.S., Gasterland, T., Marsawa, Y., Lechard, B., Dyons, J., May, B., M., Karochkin, I.V., Lee, Y., Lehard, B., Lyons, F., Nangiott, D.R., Waltais, L., Massawa, Y., Reddiersky, R., King, B.L., Konagaya, A., Karochkin, I.V., Lee, Y., Lehard, B., Lyons, F., Nangiott, D.R., Waltais, L., Marchionni, J., Nekeriste, J., H., Nagashima, T., Numata, K., Okido, T., Zevola, Y., Derrest, S., Freagale, F., Perrovsky, N., Pilai, R., Pontius, J.J., 10, Perrost, M., Sandelin, A., Schneider, C., Semple, C.A., Serou, M., Yang, H., Yang, L., Yang, L., Yang, L., Yang, L., Wang, Y., Watanabe, Y., Wall, M., Sandelin, A., Schneider, C., Semple, C., Warando, K., Sultana, R., Mahlestedt, C., Wang, Y., Maranabe, Y., Wall, H., Sato, K., Walter, K., Walleran, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Shinagawa, A., Hayatsı, M., Waterston, R., Lander, K., Shinagawa, A., Hayatsı, Y., Sakai, Y., Sakai, Y., Sakai, W., Maranabe, Y., Itoh, M., Kagawa, I., Maranaki, Y., Rakaa, T., Kawai, J., Sakai, W., Maranabe, Y., Rakawa, T., Kawai, Y., Sakai, Y., Sakai, Y., Sakai, Y., Sakai, Y., Sakai, Y., Sakai, W., Sakai, W., Sakai, W., Sakai, W., Sakai, Y., Sakai, Y
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-3045, Japan 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-3045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,C., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Chsato,N., Saito,R., Sakazume,N., Takeda,Y.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                            7-DEC-2002
musculus
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.
                                                                                                                                                                                                                                           ear
                                                                                                                                                                                                                  linear
                                                                                                                                                                                                         BY752739 mRNA
BY752739 RIKEN full-length enriched, adult cDNA clone F930014106 5', mRNA sequence.
BY752739
BY752739.1 GI:27183802
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                               musculus
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PUBMED
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TITLE

COMMENT

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Computer-based methods for the mouse full-length cDNA conputer-based methods for the mouse full-length cDNA construction of a encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 2.7e-69;
0; Mismatches 87;
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="F930014I06"
/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length er
a 133 c 171 g 168 t
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1 Similarity 82.7%;
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Mus musculus

Mus musculus

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 500)

8 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

8 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

8 Marra,M., Hillier,L., Theising,B., Allen,M., Bowers,Y., Person

8 Marra,M., Steptoe,M., Tape,D., Harvey,N., Schurk,R., Ritter

8 F., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

7 Materston,R. and Wilson,R.

7 Materston,R. and Wilson,R.

7 Materston,R. and Wilson,R.

7 Materston,R.

8 Materston,R
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/tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (karamycin_resistant)"
/clone_lib="Stratagene mouse testis (#937308)"
/note="Organ: testis; Vector: pBluescript SK-; Si:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Proligo dT. Average insert size: 1.0 kb; Uni-ZAP XR-5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' ad sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:307801
This read is a RESEQUENCE of a previously sequenced mouse This read has been verified (found to hit its original seleorrect orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 339.
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      sednerce
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10096"
/clone="IMAGE:513953"
   mRNA
KINASE KKIALRE (HUMAN);, mRNAI385966
AI385966.1 GI:4199429
EST.
Mus musculus (house mouse)
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| . . 824
| /organism="Gallus gallus"
| /mol type="mRNA"
| /strain="White Leghcrn, Hisex"
| /strain="White Leghcrn, Hisex"
| /db xref="taxon:9031"
| /clone="ChEST66113"
| /tissue type="whole embryo"
| /dev stage="20-21"
| /lab_host="DH108"
| /clone lib="CSEQCHN04"
| /clone lib="CSEQCHN04"
| /clone lib="CSEQCHN04"
| /note="Organ: whole embryo; Vector: pBluescript II KS(+);
| Site l: EcoRI; Site 2: Not1; This normalized library was constructed from I million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.
| Following this first strand reaction, double-stranded CDNA was blunted, ligated to NotI adapters, digested with EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 counds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1994) 91: 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BU221831
603750354F1 CSEQCHN04 Gallus gallus cDNA clone ChEST661113 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae;
419 GGCCGTCGGCTGTGTTTATGCAGAGCTTCTGACGTGTCAGCCACTCTGGCCCGG-AAATA
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1 (bases 1 to 824)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

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Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO Box 88, Manchester, M60 1QD, 1
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk
Location/Qualifiers
1. .824
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Gallus gallus
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ml34h09.rl Stratagene mouse testis (#937308) Mus musculus cDNA
clone IMAGE:513953 5' similar to gb:X66358 SERINE/THREONINE-PROTEIN
AA061797.1 GI:1555606
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 938)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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        824
        Length
                      Indel
         231;
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D
       Score 319.4; Pred. No. 3e-60
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       33.8%;
il Similarity 67.2%;
483; Conservative
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                                                                                                   contact the
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                                                                                                                                                                                                                                                                                                                                                                       938;
The WashU-HHMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
WashJ-HHMI Mouse EST Project
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Fmail: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; consortium (info@image.llnl.gov) for further info@is 307801
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 442.
Location/Qualifiers
ce
                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                  Score 316.8; DB 9;
Pred. No. 1.2e-59;
0; Mismatches 77;
                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:513953"
/sex="males"
                                                                                                                                                                                                                                                                                                                                                                     33.5%;
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398; Conservative
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Cy 548 ATATATGGGCTATTGGTTGTG	NO N	source 1597 /organism="Cio/mol_type="mRN/db_xref="taxc/clone="ciad64/clone="ciad64/clone_type="yo/dev_stage="yo/clone_lib="No-mol_ti"	BASE COUNT 184 a 100 c 1 CRIGIN Query Match Best Local Similarity 71.0%; F Matches 397; Conservative 0;	38 2	9 6 6 8	QY	Oy 182 CAAATCTTGTGAACCTCATCC	242 AATACTGTGATCATACACTTT	Oy 302 GAGTGATCAAAAGCGTATTA1	2y 362 ACTGTATTCACAGAGATATAN
86182 86182 Nori Satch estinalis CDNA cl 86182 86182,1 GI:19475 na intestinalis na intestinalis aryota; Metazoa; ebobranchia; Cion (bases 1 to 598) 5h,N., Satcu,Y., ressed genes in C ablished	of Zoclogy trsity (yoto, Kyoto 606-8502, Japan 753-4081 705-1113 h@ascidian.zcol.kyoto-u.ac.jp. cation/Qualifiers .598 vrganism="Ciona intestinalis" hol_type="mRNA" lb_xref="taxon:7719" ilone="cilv41b18" issue_type="whole animal" lev_stage="larva"	/clone_lib="Nori Satoh unpublished cDNA_library, larva_lip a 105 c 149 g 165 t 179 a 105 c 149 g 165 t 165 t 179 a 12.5%; Score 306.8; DB 9; Length 598; al Similarity 70.7%; Pred. No. 1.8e-57; 423; Conservative 0; Mismatches 172; Indels 3; Gaps_lip_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_arage_ara	ATGAGAAGATAGGTAAGATTAAAAAATTTGTGGAATCTGAAGATGTCGGAACC AAACCTCTGGACAAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGATGTCCTGTTG GTGACTCGGGACAAATTGTGGCAATCTGAAGATGACCTGTTG GTGACTCGGGACAAATTGTGGCCATCAAAAATTTGTCGAGTCAGAAGATGACCCGCTGA	31 TTAAGAAATAGCACTAAGAGAATACGTATGTTGAAGCAATTAAAACATCCAAATCTTG 19 	91 TGAACCTCATGAGGTTTCAGGAGAAAAGGAAATGCATTTAGTTTTGAATACTGTG 2	251 ATCATACACTTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGATGGAGTGATCA 310 	311 AAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACTTAACTGTATTC 370 	371 ACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCAAGATTTGTG 430 	431 ACTICGGGTTIGCACAAATICIGATICCAGGAGAIGCCTACACCGATTATGIAGCIA 487 	488 CGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAGATACTCAGTATGGTTCTTCAGTCG 547
LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL COMMENT	FEATURES	BASE COUNT ORIGIN Query Mate Best Loca Matches	3 8 8 8	ç ç	င် ရှိ	රු සි	č d	SS GG	çy Dp	S da

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TGTTTTTGCAGAGCTCCTGACAGGCCAGCCACTGTGGCC
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91 GCTGTTAAAAATTTGTGGAATCTGAAGATGCTCTGTTGTTAAGAAATAGCACTAAGA 150	CCAAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCCAACA 33 CGCATGGAGTTAACGATGAACTCATAAAGAAAATTATTCAATTG 30 AATTTCTGTCATATACATAACTGTATTCACAGAGATATAAAAACCTGAA 39 AATTTCTGTCATATACATAACTGTATTCACAGAGATATAAAAACCTGAA 36 AATTTCTGTCACAGTCACAAATGTATTCACAGAGATTTGCACAAATT 450 AATTTCTGTCACAGTCACAAATGTATTCACGAGATTTGCACAAATT 450 ACTAAGCAAGGAATAATCAAGATTTGTGACTTCGGGATTTGCTCGAATA 42 ACTAAGCAAGGAATAATGTAAGCTACGAGATTTGGGATTTGCTCGAATA 42 BATGCTACACCGATTATGTAGCTACGAGATGTTGGGTTCCTGAA 48 BAAATGTAATGGTTCTTCAGTCGATATATGGGCTGTAGGTTGTT 57 BAAATGTAATGGGCCACCTGTAGACATTTGGGCTGTAGGATGTT 57 BAAATGTACTCAATAGGGCCACCTGTAGACATTTGGGTTAGGTT 57 BAAATGTACTCAATAGGCCACCTGTAGACATTTGGGTTAGGTTA 54 BAAGTTCAATAGGGCCACCTGTAGACATTTGGGTTAGGTTA 54 BAAGTTCAATATGGGCCACCTGTAGACATTTGGGTTAGGTTA 54 BAAGTTCAATATGGGCCACCTGTAGACATTTGGGTTAGGTTA 54 BAAGTTCAATATGGGCCACCTGTAGACATTTGGGTTAGGTTA 54 BAAGTTCAATATGGGCCACCTGTAGACATTTGGGTTAGGTTA 54 BAAGTTCAATATGGGCCACCTGTAGACATTTGGGTTAGGTTA 54 BAAGTTCAATATGGGCCACCTGTAGACATTTGGGTTAGGTTAGTTA	AW106692 um32d03.yl Sugano mouse kidney m IMAGE:223629 5' similar to gb:x KINASE KKIALRE (HUMAN);, mRNA se AW106692.1 GI:6077492 EST. Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Cr Mammalia; Eutheria; Rodentia; Sc 1 (bases 1 to 731) Marra, M., Hillier, L., Kucaba, T., Underwood, K., Steptoe, M., Theisi , B., Swaller, T., Gibbons, M., Pap , E., Kohn, S., Shin, T., Jackson, Y Waterston, R. and Wilson, R. The Washington University School of 4444 Forest Park Parkway, Box 85 Tel: 314 286 1810 Email: mouseest@watson.wustl.edu	This clone is available royalt IMAGE Consortium (info@image.1 MGI:1006441 Seq primer: custom primer used High quality sequence stop: 43 Location/Qualifiers 1731 /organism="Mus muscul /mol_type="mRNA"
ap da	S S S S S S S S S S S S S S S S S S S	RESULT 13 AMID6692 LOCUS DEFINITION VERSION VE	FEATURES
422 AGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATT 478 []	CB400506 CB400506 CB400506 CB400506.1 GI:30742 EST. Caenorhabditis elega Caenorhabditis elega EST. CAENORHABDITIS elega EVARYOTA; METAZOA; RBADDITIS elega EVARYOTA; METAZOA; REBOUL, J., VAGIIO, P., C.M., Li,S., Jacoto J.R., Hartley, J.L., Endress, G.A., Jenna, PEACEK, J., Snyder, Doucette-Stamm, L., H C. elegans ORFeome v genome annotation an expression LNAL. Genet., (2003) CONTACT: Vidal M	Tarc volume Tel: 6 Fax: 6 Fax: 6 Clonir Carolidary Colonir Carolidary Colonir Carolidary Colonir Carolidary Colonir Carolidary Colonir Carolidary Colonir Carolidary	Y Match Local Similarity 67.6%; Pred. No. 2.8e-49; Since 379; Conservative 0; Mismatches 182; Indels 0; Gaps C; 31 GGAGAAGGGTCTTATGGGGTTGTATTCAAATGCAAAACCTCTGGACAAGTAGTA 90
20 CO	RESULT 12 CB400506 LOCUS DEFINITION ACCESSION VERYWORDS SCURCE ORGANISA AUTHORS AUTHORS TITLE COMMENT	FEATURES sour sour	Query Best 1 Matche Qy Db

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09-671-050-11

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27.0%; Score 255; DB 14;
larity 63.5%; Pred. No. 5.3e-46;
Conservative 0; Mismatches 230;
            GI:24552933
                                  Homo sapiens (human)
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/clone_lib="Sugano mouse kidney mkia"
/clone_lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site_i: Drail!
(CACTGTGTGT); Site_2: Drail! (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a Drail! adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct Drail! sites of the pWE18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xho! should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACACA."

2 others
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8.5 EPT Homo sapiens CDNA
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Pred. No. 8.7e-47;
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NISC lt01h12.yl COGENE
IMAGE:5605870 5', mRNA
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        /db_xref=
/clone="I
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5605870"
/tissue_type="embryo, 8 weeks postconception"
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/note="Vector: pAMPl; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMPl. Size
selected for insert sizes ranging from 0.2-2.5 kb.
Normalized to CotlO. Primary library, non-amplified.
Library constructed by M. Lovett. For more information this library, please contact R. Tidwell (Washington University) or visit the COGENE website at
http://hg.wustl.edu/COGENE/."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation:
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM12404 row: O column: 23
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Xarra,X., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennen,G., Soares,B., Wilson,R. and
Waterston,R.

The WashU-HHMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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vc33b05.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE:
similar to gb:X66358 SERINE/THREONINE-PROTEIN KINASE KKTA)
); mRNA sequence.
AA286088
AA286088.1 GT:1932198
EST.
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; conta
IMAGE Consortium (info@image.llnl.gov) for further inform
MGI:469193
                                                                                                                                CAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTT
                                                                                                                                                                                 Seq primer: -28ml3 rev2 ET from Amersham
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Location/Qualifiers
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/lab_host="DH10B"
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Sequence 5, Application US/09411628

Patent No. 6428994

GENERAL INFORMATION:

APPLICANT: University of Southern California

IITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN

IITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

CURRENT FILING DATE: 1999-10-01

EARLIER APPLICATION NUMBER: US 60/102,906

EARLIER FILING DATE: 1998-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 9.1e-61;
; Mismatches 237;
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US-08-781-891-79
US-09-618-166-79
US-09-791-211-3
US-09-798-096-10
US-09-798-096-3
US-09-851-896-3
US-09-851-896-3
US-08-750-703-4
US-08-750-703-4
US-09-740-041-3
US-09-659-845A-22
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Pred. No. 2.7e-36;
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; Patent No. 5863741
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Thomas, Charles F.
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 330(2)
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-288-9696
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MOLECULE TYPE:
FEATURE:
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US-C8-874-347-9
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                                                    3080
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Patent No. 6428994

GENERAL INFORMATION:

APPLICANT: University of Southern California

TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

CURRENT FILING DATE: 1999-10-01

EARLIER APPLICATION NUMBER: US 60/102,906

EARLIER FILING DATE: 1998-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 3080
                                                                                                                                                                                           Score 251.8; DB 4;
Pred. No. 1.2e-60;
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Conservative
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Best Local Similarity
Matches 407; Conser
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; LOCATION: (249)
US-09-411-628-3
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US-09-411-628-3
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Pred. No. 2.7e-36;
); Mismatches 287;
                                PRIOR APPLICATION:

APPLICATION DATA:

APPLICATION NUMBER: 08/874,347

FILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ellinger, Mark S.

REGISTRATION NUMBER: 34,812

REFERENCE/DOCKET NUMBER: 07039/055002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-335-5070

TELETAX: 612-288-9696
  APPLICATION DATA:
TATION NUMBER: US/09/093,
DATE: 08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                   :0
                                                                                                                                                                                                                                                             LOCATION: 1...900
; OTHER INFORMATION:
US-09-093-522-9
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Best Local Similarity 55.2%;
Matches 365; Conservative
                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
               APPLICATION NUMBER FILING DATE: 08-UT CLASSIFICATION:
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FEATURE:
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US-09-093-522-9

Sequence 9, Application US/09093522

Patent No. 6015700

GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Thomas, Charles F.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FF
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CCRRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 330
CITY: Minneapolis
STATE: MN
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FastSEQ for
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OPERATING SYSTEM:
SOFTWARE: FASESE
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Sequence 1, Application US/39338125
; Satent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATA:
>: US/09/338,125
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R: 7934-057
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 793
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: nucleic acid
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ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/08/FILING DATE:
APPLICATION NUMBER: US/08/FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS:
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US-09-338-125-1
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AAGCCATTATTTCCAGGTGATTCTGAAATTGATGAAATATTTAGAATATTTAGAATATTA 660
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Pred. No. 1.1e-35;
); Mismatches 290;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,10
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lesie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-0
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
CFOITENCE CHARACTERISTICS:
                                                                                                                               Sequence 1, Application US/08969106; Patent No. 5986055; GENERAL INFORMATION:
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.; TITLE OF INVENTION: CDK2 INTERACT:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Amer CITY: New York
STATE: New York
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Best Local Similarity 55.0%;
Matches 362; Conservative
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LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1...894
OTHER INFORMATION:
S-08-969-106-1
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US-08-969-106-1
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SEQ ID NO 13
LENGTH: 1476
TYPE: DNA
ORGANISM: Homo
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US-09-266-225D-13

Sequence 13, Application US/09266225D

Patent No. 6573364

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishan

APPLICANT: Kingsmore, Stephen

APPLICANT: Tchernev, Velizar

TITLE OF INVENTION: Isolation and Characterization of Hei

TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and

TITLE OF INVENTION: Interacting Proteins

FILE REFERENCE: 15966-523
                                                                     Score 162; DB 4; I
Pred. No. 1.1e-35;
); Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 15966-523
CURRENT APPLICATION NUMBER: US/09/266,225D
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 55.0%;
Matches 362; Conservative
                        NAME/KEY: Coding Se
LOCATION: 1...894
OTHER INFORMATION:
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         MOLECULE TYPE:
TOPOLOGY:
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                                                           Length
                                                     Score 162; DB 4;
Pred. No. 1,1e-35;
; Mismatches 290;
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US-09-417-197-112
Sequence 112, Application US/09417197
Patent No. 6518021
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: On A Cellular Response
TITLE OF INVENTION: On A Cellular Response
TITLE OF INVENTION: On A Cellular Response
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
SEQ ID NO 112
LENGTH: 1635
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US-09-220-132-3
; Sequence 3, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: METHODS AND COMPOSITONS
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR PPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                             d. No. 1.16
Mismatches
                                                                                Score 162;
Pred. No. 1
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55.0%;
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                                                                                          Local Similarity 55.0
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    INFORMATION:
                FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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                                                                              Score 162; DB 4;
Pred. No. 1.1e-35;
0; Mismatches 290
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US-09-417-197-114
Sequence 114, Application US/09417197
Patent No. 6518021
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
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Best Local Similarity 55.0%;
Matches 362; Conservative
  INFORMATION: CDK2-EGFP
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OTHER INFORMAT
FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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LENGTH: 1635
TYPE: DNA
ORGANISM: Art
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1 Similarity 52.4%;
345; Conservative
 Jian-Rui
                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (234)..(1235)
-09-620-312D-313
                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Best Local S
Matches 345
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                                   Score 154.2; DB 4;
Pred. No. 1.4e-33;
; Mismatches 293;
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Sequence 313, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
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ilarity 54.3%;
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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Pred. No. 4.8e-28;
                                                                                                             Acids
                                                                                                             Nucleic
APPLICANT: Mang, clan-kul
APPLICANT: Zhou, Ping
APPLICANT: Wang, Durrui
APPLICANT: Wang, Durrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
CURRENT PRICATION: POlypeptides
FILE REFERENCE: 784CIP2B
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL Genes Version 1.0
SEQ ID NO 313
LENGTH: 1825
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RESULTUS-08-

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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-464-517-37

JS-08-464-517-37

Sequence 37, Application US/08464517

Patent No. 5869640

GENERAL INFORMATION:

APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN.

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA
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nes 308;
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Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C7/963,308
FILING DATE: 16-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
                                                                                                                                             Cyclin Complex Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MI-626
                                                                                                                                                                                                                                                                                                                                                                            MBER: US/08/154,91
19-NOV-1993
                                                                                                               APPLICANT: Beach, David
APPLICANT: Xiong, Yue
TITLE OF INVENTION: Cyclin Comple
TITLE OF INVENTION: Related There
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                           IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
                                                                     Sequence 1, Application US/0815491
Patent No. 5618669
GENERAL INFORMATION:
APPLICANT: Beach, David
APPLICANT: Xiong, Yue
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larity 52.3%;
Conservative
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Floppy disk
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA
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344; Conserv
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LOCATION:
S-08-154-915-1
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Pred. No. 1.1e-
0; Mismatches
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227-7400
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52.3%;
         TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                            1089 base pairs
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344; Conservative
                                                                    double
                                                         nucleic acid
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TOPOLOGY: 1
                                                                                         MOLECULE TYPE:
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LOCATION:
8-464-517-37
                                             LENGTH:
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CYCLIN AND USES RELATED THERETO

COCKFIELD

APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKE

Sequence 37, Application US/08246361A Sequence 37, Application US/08246361A Patent No. 5998582 GENERAL INFORMATION:

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Pred. No. 1.1e-27;
; Mismatches 308;
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ATTORNEY/AGENT INT.

NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                         SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
                                                                                               MBER: US/08/246,361A
19-MAY-1994
                                                                                                                                                                                                               FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
             MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 52.3%;
Matches 344; Conservative
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 16-MAY-1991 ATTORNEY/AGENT INFORMATION:
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            COMPUTER READABLE MEDIUM TYPE: FI
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US-08-246-361A-3
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Pred. No. 1.1e-27;
0; Mismatches 308;
                                                                                                                                                                                                                                                                                                                                                                                MEDIUM IIEE: FICEDY COMPUTER: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-DO4C
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
FENCTUS 1089 bace paire
                                                                                                                                                                                                 US-08-463-772-37

Sequence 37, Application US/08463772

Patent No. 6066501

GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN:
TITLE OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%;
Similarity 52.3%;
14; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION:
JS-08-463-772-37
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Bos taurus (cow)

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

Est (Adelson and Gill; C.A.

Bovine ESTE (Adelson and Gill)

Contact: David L. Adelson

Animal Breeding and Genetics

Texas A&M University

Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,

USA

Tel: 9798452616

Fax: 9798456970

Email: david.adelson@tamu.edu.

Location/Qualifiers

Location/Qualifiers

Lorganism="Bos taurus"

source

FEATURES

RUC663000 BY733578 BY752739 ml34h09.y

CB169554 BY733578 BY752739 AI385966 m

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BY733578 RIKEN full-length enriched, 16 days neonate mal diencephalon Mus musculus cDNA clone G630052E12 5', mRNA BY733578.

G1:27146705

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur (bases 1 to 670)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imctani,K.,
,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imctani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
L Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Shii,Y., Itoh,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 689)
S Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bcno,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
Jarvis,E.D., Kanai,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,
,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
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enriched, adult inner
mRNA sequence.
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                                                                enriched,
                                                                                                                                                               Score 405; DB 14;
Pred. No. 1.8e-17;
0; Mismatches 76;
                                       /dev_stage="16 days neonate"
/clone_lib="RIKEN full-length
male_diencephalon"
nale_140 c 169 g 155 t
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BY752739 RIKEN full-length enriceDNA clone F930014I06 5', mRNA BY752739

BY752739.1 GI:27183802
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Computational Analysis of Full-Length Mouse cDNAs Compared with Fuman Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Eutheria: Rodentia: Sciurognathi; Muridae; Musinae; Mus
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Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933411017 product:cyclin-dependent kinase-like 1 (CDC2-related kinase), full insert sequence.

AK016781

AK016781

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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                /organism="Mus musculus"
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/clone="IMAGE:513953"
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/tissue_type="testis"
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 500)

S Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Materston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

Unpublished

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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mRNA linear EST 27-JAN-1999
ml34h09.yl Stratagene mouse testis (#937308) Mus musculus cDNA
clone IMAGE:513953 5' similar to gb:X66358 SERINE/THREONINE-PROTEIN
KINASE KKIALRE (HJMAN);, mRNA sequence.
A1385966.1 GI:4199429
EST.
Mus musculus (house mouse)
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Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LINL; contactions of the consortium (info@image.llnl.gov) for further information (info@image.llnl.gov).
ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTAT
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Seq primer: -40RP from Gibco High quality sequence stop: 33 Location/Qualifiers
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/db_xref="MG1:1918341"
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kinase-like_1 (CDC2-related kinase) (MGD/MGI:1918341)
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/db_xref="taxon:10090"
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Analysis of the mouse transcriptome based on functional annotatio of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1691)

8 Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,E., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Arakawa,T., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,W., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Numazaki,R., Ohno,M., Ckazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
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Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 938)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

The Washu-HHMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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ml34h09.rl Stratagene mouse testis (#937308) Mus musculus clone IMAGE:513953 5' similar to gb:X66358 SERINE/THREONIN KINASE KKIALRE (HUMAN);, mRNA sequence.
AA061797
AA061797.1 GI:1555606
EST.
Mus musculus (house mouse)
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Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; conta

IMAGE Consortium (info@image.llnl.gov) for further inform

MGI:307801

Seq primer: -28m13 rev1 ET from Amersham

High quality semiones
AAGATITGIGACTICGGGTTIGCACAAATICTGATT---.CCAGGAGATGCCTACA
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/note="Organ: testis; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
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Av986182

Av986182

Nori Satch unpublished cDNA library, larva Ciointestinalis cDNA clone cilv41b18 5', mRNA sequence.

Av986182.1

Av986182.1

GI:19475050

EST,

Ciona intestinalis

Satch,N., Satcu,Y., Kohara,Y. and Shin-i,T.

Expressed genes in Ciona intestinalis

Unpublished
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                                                                                                              Score 316.8; DB 9;
Pred. No. 5e-12;
0; Mismatches 77;
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Location/Qualifiers
1. .598
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/mol_type="mRNA"
/db_xref="taxon:7719"
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Contact: Nori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 6
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                               30.4%;
imilarity 82.9%;
; Conservative
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GIGGGAGATACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTTTTTGCA
   Sciences
  of Biomolecular Sciences of Manchester Institute
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il Similarity 68.7%;
426; Conservative
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603750354F1 CSEQCHN04 Gallus gallus cDNA clone ChEST661113 sequence.
BU221831
BU221831.1 GI:25410266
EST.
Gallus gallus (chicken)
Gallus gallus (chicken)
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
El (bases 1 to 824)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbarc Curr. Biol. 12 (22), 1965-1969 (2002)
E 22335534
Curr. Simon Hubbard
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165 t
                                                         Score 306.8; DB 9;
Pred. No. 2.7e-11;
0; Mismatches 172;
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g l
/clone="cilv41b18"
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/clone_lib="Nori Sato
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                                                         29.5%;
ilarity 70.7%;
Conservative
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/strain==white Leghorn, Hisex"
/db xref=="taxon:9031"
/clone=="ChEST66113"
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/lab_host==nD4.0B"
/clone lib=="CSEQCHNO4"
/constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand reaction.
/constructed from 1 million independent clones. cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
/compatible sites of a custor modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
/counds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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      LSIMD)
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Pred. No. 7.5e-11;
0; Mismatches 191;
of
                                          FO Sox 88, Manchester, M6C 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. 824
/organism="Galius gallus"
/mol_type="mRNA"
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RESULT 9 BU686325/c LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED

FEATURES

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BP016186

BP016186 Nori Satch unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciad64e08 5', mRNA sequence.

BP016186

BP016186.1 GI:19507663

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/mol_type="mRNA"
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Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ase
Eukaryota; Metazoa; Chordata; Urochordata; Ase
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 597)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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Pred. No. 3.4e-10;
0; Mismatches 159;
                                                         Score 295.6; DB 13
Pred. No. 1.4e-10;
); Mismatches 4;
    187
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//dev_stage="DH10B (Life Technologies) (T1 phage resistant)"
//dev_stage="DH10B (Life Technologies) (T1 phage resistant)"
//dove="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
//note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
//incf-Du1 is a normalized_cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The following tissue(s): Primary Lung Epithelial Cells Tissue normalized containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, disgested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleoride used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)!B tail. The sequence tag for this library is GGTTGTAGC.

TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-36B TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-36B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa
University of Iowa
University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa
2024 University of Iowa
2024 University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.
                                        636
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 536)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate g discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: McCray, PB

McCray Lab
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UI-CF-DU1-adn-i-10-0-UI.S1 UI-CF-DU1 Homo sapiens cDNA clu
UI-CF-DU1-adn-i-10-0-UI 3', mRNA sequence.
BUG86325
BUG86325.1 GI:23541120
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GTGGGGGACACGCAGTATGGCCCTCCTGTGGACGTGTGGGCAATAGGCTGTGTCT
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/db_xref="taxon:10116"
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/tissue_type="Pitutary"
/lab_host="DH10B"
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and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.23 kb (range 0.5-4.C kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by clontech
laboratories (Palo Alto, CA)."
1988 c 200 g 202 t lothers
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CB400506

CB400506.1 G:

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                                    CB315C94

ON AGENCOURT 11526413 NICHD RI Pitl Rattus norvegicus CDNA clone IMAGE:6888377 5', mRNA sequence.

N CB315O94

CB315O94

CB315O94.1 G1:28838974

CB315O94.1 G1:28838974

EST.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

E 1 (bases 1 to 825)

S NCI-COAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP Tunor Gene Index

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L Orpublished

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Tissue Procurement. John C. Marshall, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: agapbs-r@mail.nih.gov

Tissue Procurement. John C. Marshall, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: agapts-rightion: Clone distribution information clound through the I.M.A.G.E. Consortium/LinL at: http://image.llnl.gov

Plate: LLCM3144 row: i column: 16

High quality sequence stop: 468.

Location/Qualifiers
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/mol_type="mRNA"
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Score 284.6; DB 14;
Pred. No. 5.5e-10;
; Mismatches 90;
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Tolias, P.P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
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/db_xref="taxon:6239"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
4 a 88 c 135 g 158 t
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Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Retazca; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

Rhabditidae; Peloderinae; Caenorhabditis.

Lhases 1 tc 565)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Arms, C.M., Li,S., Jacctot, L., Bertin, N., Janky, R., Moore, T., Hudsc, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of tygenome annotation and resource for proteome-scale protein expression

Nat. Genet., (2003) In press

Contact: Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA C2115, USA

Tel: 617 632 5189

Fax: 617 632 5189

Fax: 617 632 5189

Email: Marc Vidal@dici.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORF Cloning project: Contact david_hill@dici.harvard.edu

Marc Vidal@dici.harvard.edu

Marc Vidal@dici.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORF. Manc Vidal@dici.harvard.edu
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Pred. No. 5.7e-09;
); Mismatches 182;
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1. .565
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/sex="female"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH10B"
/clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney; Vector: pME18S-FL3; Site_l: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor {TGTTGGCCTACTGG}, digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                           AW106692

UM32d03.yl Sugano mouse kidney mkia Mus musculus cDNA clone
INAGE:2236229 5' similar to gb:X66358 SERINE/THREONINE-PROTEIN
AKINASE KKIALRE (HUMAN);, mRNA sequence.
AW106692.1 GI:6077492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 731)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,E., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                             570
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1006441
Seq primer: custom primer used
                                                                                                                                                                                        High quality sequence stop: 433.

Location/Qualifiers

1. 731

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2236229"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠.
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; c
IMAGE Consortium (info@image.llnl.gov) for further ir
MSI:469193
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 424.
Location/Qualifiers
1. 718
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10096"
/clone="IMAGE:776337"
/cox="mixed"
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                                                                             further
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Pred. No. 4.2e-08;
0; Mismatches 190;
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l Similarity 67.9%;
416; Conservative
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Mus musculus
Mus musculus

Mus musculus

Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashJ-HHMI Mouse EST Project
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vc33b05.rl Barstead MPLRB1 Mus musculus cDNA clone IN similar to gb:X66358 SERINE/THREONINE-PROTEIN KINASE);, mRNA sequence.
AA286088.l GI:1932198
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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AA286388
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Innovation
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/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoRl;
Site_2: Notl; The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups. "
                                                                                                                                                                            BIS11582
BB160006A20C12.5 Bee Brain Normalized Library, BB16 Apis mellifers CDNA clone BB160006A20C12 5', mRNA sequence.
BIS11582
BIS11582.1 GI:15361956
EST.
Apis mellifera (honeybee)
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r studie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Criti
Research Initiatives Fund and a Burroughs-Wellcome Trust Inr
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                                                                                                                                                                                                                                                                                                                                                                                    Apidae; Apis.

1 (bases 1 to 508)
Whitfield, C.W., Band, M.R., Bcnaldo, M.F., Kumar, C.G., Liu, J. Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E. Annotated expressed sequence tags and cDNA microarrays for brain and behavior in the honey bee Genome Res. 12 (4), 555-566 (2002)
21929762
11932240
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647 ICCCCCTGIAGAIGICIGGC-AAIGGCIGIGITIGCIGAGIIACIGICCGGA
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/dev_stage="adult worker honey bee"
/lab_host="DH108"
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Pred. No. 1.2e-37;
); Mismatches 160;
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BACKWARD: ATTAACCCTCACTAAAG
Plate: BB160006A20 row: C column: 12
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 508.
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/crganism="Apis mellifera"

/mol_type="mRNA"

/strain="mixed strains of E

A.m. ligustica"

/db_xref="taxon:7460"

/clone="BB160006A20C12"

/sex="female"
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Best Local Similarity 68.3%;
Matches 345; Conservative
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MEDLINE
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                                                                               GAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCT
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18-09

Human kinase 14257
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DNA encoding novel
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AAI 64248
ABX34679
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ABZ77165
AAA29746
AAA297476
AAA377835
AAA71073
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AAA7762483
AAA71085
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generating r screening for medical diseases

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New isolated human kinase polynucleotide useful for gantibodies, as reagents in diagnostic assays and for compounds useful for treating mental, biological or m
                                                      Claim 3; Page 33; 38pp; English.
                 WPI; 2001-266166/27.
                       P-PSDB; AAE03495
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The present sequence is a cDNA encoding novel human protein

(NHP) known as human kinase. The human kinases share structural

similarity with animal kinases, more particularly serine or

threonine protein kinases. Human kinase cDNA is useful for the

detection of mutant human kinase for the diagnosis of disease,

and also as a therapeutic. It is useful for screening drugs

effective in the treatment of symptomatic or phenocypic

manifestations perturbing the normal function of NHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

identification of other cellular gene products related to human

kinases, and as reagents in assays for screening compounds that

are useful for treating mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics and pharmacogenomics. Nucleotide construct

encoding NHP products are used to genetically engineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

encoding nor functions in the body. Nucleotide constructs
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mental bioreactor; m 97 Human; kinase; gene therapy biological disorder; ss. CDNA; standard; CDNA Human kinase 9-JUN-2001 57 4 3814 AAD03814

stop include not does "Human kinase #3" se coding region d Location/Qualifiers 1..972 /product = "Ht
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/partial 1..97; /*tag Key

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The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the antibodies, as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide constructs in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP encoding encoding functional NHPs are used in gene therapy for the
                                                                                                                      New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening foompounds useful for treating mental, biological or medical dise
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                                                WPI; 2001-266166/27
P-PSDB; AAE00492.
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expression.

96; 972; Indels Length ·; Score 823; DB 22; Pred. No. 3.3e-210; 0; Mismatches 0; 0; 79.1%; ilarity 90.6%; Conservative Query Match Best Local Similarity Witches 929; Conserv

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CDNA polypeptide (PKIN-10) ВР CDNA; 1790 entry) (first standard; Humar kinase 21-MAY-2002 AAD30557 SULT

Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; choiestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic; hypotensive; anti-HIV; enzyme; ss.

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"Human PKIN-10 Location/Qualifiers 239..1267 /*tag= a /product= "Human PK]

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Human; ss; gene; diagnostic and therapeutic; DITHP; cancer; arteriosclerosis atherosclerosis; psoriasis; primary thrombocytopenia autoimmune; inflammatory; anaemia; asthma; autoimmune thyroiditis; Crohn's disease; diabetes mellitus; glomerulonephritis; gout; stroke; multiple sclerosis; rheumatoid arthritis; uveitis; AIDS; allergy; acquired immunodeficiency disease; neurological disorder; epilepsy; Alzheimer's disease; dementia; mental retardation; gastrointestinal; Parkinson's disease; ulcer; cirrhosis; reproductive; infertility;
                         AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT
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                                                                                                                                                                                                                                                                                                           The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, 17mphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis), a growth and developmental disorder (e.g., atherosolerosis, hypertension, myocardial cardiovascular disorder (e.g., fatty liver, cholestasis, cardiovascular disorder (e.g., fatty liver, cholestasis, danaering techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting chifferences in the chromosomal location due to translocation, inversion, grobes for mapping naturally occurring genomic sequences. PKIN is useful in southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays and in microarrays utilising tinked immunosorbent (ELISA)-like assays and in microarrays utilising present sequence is human PKIN-10 obbMa.
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Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Bandman O, Nguyen DB, Lu Y, Burford N, Lal P;
MG, Elliott VS, Recipon SA, Kearney L, Lu DAM;
Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J;
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Pred. No. 1.4e-209;
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                         2000US-2220138P.
2000US-222112P.
2000US-222831P.
2000US-224729F.
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Matches 927; Conservative
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P-PSDB; AAE19152.
                         21-JUL-2000;
28-JUL-2000;
04-AUG-2000;
11-AUG-2000;
  20-JUL-2001;
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2001US-261864P.
2001US-261865P.
2001US-262264P.
2001US-262268P.
2001US-262209P.
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2001US-263209P.
2001US-263063P.
2001US-263065P.

(INCY-) INCYTE GENOMICS

es en P F F F F Dufour GE, Hillman JL, V, Daffo A, Marwaha R, David MH, Lewis SA; Altus CM, s B, Flores Peralta CH, Lincoln SE, A iu TF, Harris E Gerstin EH, Pe SR, Liu Ge SC,

2003-040686/03 P-PSDB; ABU05290 New human diagnostic and therapeutic (DITHP) polynucleotides and polypeptides, useful for diagnosing, preventing or treating disease; e.g. cancer, AIDS, Parkinson's disease, or autoimmune/inflammatory e.g. cand diseases

Claim 1; Page 267; 331pp; English.

This invention relates to the cDNA and protein sequences of fifty six polynucleotides for diagnostics and therapeutics (DITHP). The human DITHP polynucleotides and polypeptides are useful for diagnosing, preventing or treating diseases associated with, as well as effects of exogenous compounds, on the expression of human molecules, such as cell proliferative diseases (e.g. cancer, arteriosclerosis atherosclerosis, proliferative diseases (e.g. cancer, autoimmune/inflammatory diseases (e.g. anaemia, asthma, autoimmune thyroiditis, Crohn's disease, diabetes mellitus, glomerulonephritis, gout, multiple sclerosis, rheumatory diseases; c.g. arthitis, uveitis, acquired immunodeficiency disease, AlDS; allergies, arthitis, uveitis, acquired immunodeficiency disease, AlDS; allergies, neurological disorders (e.g. stroke, Alzheimer's disease, dementia, mental retardation, Parkinson's disease, epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. infertility, endometricsis), endometrics, confections (e.g. bacterial, hyperlipidemia, obesity), connective tissue disorders (e.g. osteoporosis, Reiter's syndrome), or infections (e.g. bacterial, viral, fungal, parasitic, protezoal). The DITHP sequences may be used to generate hybridisation probes useful in chromosomal mapping of naturally occurring genomic sequences. They are also useful in diagnostic assays. The polynucleotides are useful as molecular weight markers, or as antigen to elicit an immune response. The present sequence represents a human diagnostics and therapeutics (DITHP) conaectory are also useful an immune response. The

0 other; .. H C; 336 G; 493 541 A; 308 BP; Sequence 1678

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Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays.

The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify
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                                                                                                                                               Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder neurodegenerative disorder; inflammatory disorder; infectious disreproductive disorder; gene therapy; ss.
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is a human kinase. A polymorphism was identified in the 3' UTR of the present sequence. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modularion of NHP canes are used in gene therapy for the
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other; : : 503 Seguence 1819 BP; 539 A; 368 C; 406 G;

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P-PSDB; AAG78547.
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The invention relates to an isolated 14257 polypeptide and nucleic acid encoding it. The 14257 protein is a protein kinase that acts as a medulating agent in regulating a variety of cellular processes, including cell proliferation, differentiation, growth and division. The activity of the protein of the invention may be described as; cytostatic; osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive; antiinflammatory; antiarthryrcid; antipsoriatic; ophthalmological; antiallergic; antiarthythmic; virucide; anorectic; metabolic; immunomodulator and antiarshythmic; virucide; anorectic; metabolic; immunomodulator and analgesic. The protein of the invention may act as a novel diagnostic target or therapeutic agent controlling certain disorders, for example kinase-associated or other 14257-associated disorders. These may include cellular proliferative disorders such as cancers e.g. acute lymphoblastic leviemia or Hodgkin's disease. Other disorders include bone metabolism disorders such as osteoporosis, disorders of the immune system, e.g. inflammatory, diabetes mellitus, osteoarthritis and asthma. Proteins of the invention may also be of use as therapeutic agents in cardiovascular disorders such as hypertension and coronary artery disease, and some endothelial cell disorders, including psoriasis. The current sequence represents a human kinase 14257 cDNA.
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ABU11450-ABU11845, described in the disclosure of the invention.

Specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; esteopathic; cytostatic; anti-HIV haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis
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ald Y, Gerstir
SR, Harris F
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Hillman JL, Yu JY, Tuason O, Yap PE, Ams
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y,
1, David MH, Lewis SA, Chen AJ, Panzer SR,
Marwaha R, Lo A, Lan RY, Jrashka ME;
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                             CDNA; 1281
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2001US-280067P.
2001US-291280P.
2001US-291829P.
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29-MAR-2001;
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17-MAY-2001;
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isease,
                                                                                                                             The present sequence encodes a novel protein kinase. The rucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and discorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the product of antibodies of kinase expression and activity. Diseases related to down regulate kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autcimmune disorders, cardiomyopathies, strokes, renal failure, number disorders, cardiomyopathies, strokes, renal failure, chronic inflammatory pelvic disease, multiple sclerosis, asthma, content of disorders, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.
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Pred. No. 1.1e-133;
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kinases, and as reagents in assays for screening compounds that

are useful for treating mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics and pharmacogenomics. Nucleotide construct

encoding NHP products are used to genetically engineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

encoding functional NHPs are used in gene therapy for the

modulation of NHP expression.
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                                                                                                                                          Score 454.4; DB 22; Length
Pred. No. 1.2e-111;
1; Mismatches 1; Indels
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note= "The coding region d
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biological disorder; ss.
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st Local Similarity 99.8%;
tches 455; Conservative
                                                                                                                          Sequence 561 BP; 189 A; 87
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(NHP) known as human kinase. The human kinases share structural

similarity with animal kinases, more particularly sexine or

threonine protein kinases. Human kinase cDNA is useful for the

detection of mutant human kinase for the diagnosis of disease,
and also as a therapeutic. It is useful for screening drugs

effective in the treatment of symptomatic or phenotypic

manifestations perturbing the normal function of NHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

continuediation of other cellular gene products related to human

kinases, and as reagents in assays for screening to a reagents in assays for screening mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics and pharmacogenomics. Nucleotide construct

cencoding NHP products are used to genetically engineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

cencoding functional NHPs are used in gene therapy for the

modulation of NHP expression.
                                                                                                                                                                                                                                      New isolated human kinase polynuclectide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases
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Pred. No. 1.2e-111;
0; Mismatches 1;
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ilarity 99.8%;
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P-PSDB; AAE00493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and/or cancers, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, cardiomyopathies, strokes, renal failure, immune disorders, cardiomyopathies, chronic inflammatory bowel disease, oxidative-stress related disorders, chronic inflammatory bowel disease, chonic inflammatory bowel disease,
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                                                                                                                                                                                                                                                                      Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory boxel disease; inflammatory boxel disease;
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cancer
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chronic inflammatory pelvic disease,
osteoarthritis, psoriasis, rhinitis,
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P-PSDB; AAB65643.
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Matches 658; Conservative
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ABZ77165
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Human; protein kinase; enzyme; antiasthmatic; antiinflammatory; antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatimmunosuppressive; vulnerary; gene therapy; CCPD; asthma; migrain chronic obstructive pulmonary disease; non-insulin dependent diapparkinson's disease; myocardial infarction; inflammatory bowel dautoimmune disorder; allograft rejection; graft versus host diseancer; leukaemia; wound granulation; gene; ss.
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                                                                                                                                                                                                                      Martinez RAM,
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06-NOV-2001;
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2001US-301098P 2001US-332870P

GENETICS

2002WC-IB02358

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                                                                                                                                  New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy fo treating e.g. Parkinson's disease, migraine, myocardial infarctiallograft rejection or cancers
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Pred. No. is the number of results predicted by chance to have

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	AX107720	Sequence 9	AX107720	AX107720.1		Homo sapie	Homo sapiens	Eukaryota;	Mammalia;	~·1	Donoho, G.,	Sands, A.T.	Human kina	
AX107720	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS		TITLE	

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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/moi_type="genomic DNA"
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Flanagan, P. and Clary, D.S. TITLE Novel human protein kinases and protein kinase-like enzymes JOURNAL Patent: WO 0138503-A 25 31-MAY-2001; Sugen, Inc. (US) FEATURES 1. 1083 Location/Qualifiers Source Location/Qualifiers Location/Quali	Obery Match Best Local Similarity 86.1%; Fred. No. 2.7e-173; Matches 927; Conservative 0; Mismatches 0; Indels 150; Gaps Oy 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 60 DD 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 60	62 TGCAGAAACCACTCTGGACAAGTAGTTGAAAAATTTGTGGAATCTGAAGAT [:::	AATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGG 	TACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT STGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT STGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT STGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCAAATAACAT TGTATTCACACAAAAAGCAAAAAAAAAA	361 AACTGTATTCACAGAGATTTGCACAAATTTCTGATAACTAAGCAAGGAATAATC 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCTAATAGCTAAGCAAGGAATAATC 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCTGATTCACATGTTGGGAGAATTGAC	TTGATGCATTT TGAGCTCCTGAA	Oy 547 GATATATGGCTATTGGTTTTTTGCAGAGCTCCTGACAGGCCAGCCA	0 + 0 + <u>H</u> -H H
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CTTCGGGTTTGCACAATTCTG	154	AX286069 AX286069 TON Sequence 3 from Patent WO0179488. ON AX286069 AX286069.1 GI:17045995 Homo sapiens (human)
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Human kinase proteins and polynucleotides encoding the Patent: WO 0123579-A 1 05-APR-2001;

Lexicon Genetics Incorporated (US)

Location/Qualifiers

ce 1. 561
/organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"

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    Martinez, R., Whyte,
                               Location/Qualifiers
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  Plowman, G.D., Martinez
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Human kinase proteins and polynucleotides encoding the sar
Patent: WO 0123579-A 7 05-APR-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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Eutheria; Primates; Catarrhini;
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join (214. .669, X66359.1:1. .54,670. .1290)
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X66358.1 GI:36614

Serine/threonine protein kinase.

Homo sapiens (human)

Homo sapiens
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Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Meyerson,M., Enders,G.H., Wu,C.L., Su,L.K., Gorka,C., Nelson,C.,
Harlow,E. and Tsai,L.H.
A family of human cdc2-related protein kinases
EMBO J. 11 (8), 2909-2917 (1992)
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Submitted (12-MAY-1992) M.L. Meyerson, Massachus
Hospital, Cancer Center, Bldg 149, 13th Street,
02129, USA
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                                                                                                     The present sequence is novel human protein

(MHP) known as human kinase. The human kinases share structural

similarity with animal kinase. The human kinase share structural

chreonine protein kinases. Human kinase cDNA is useful for the

detection of mutant human kinase for the diagnosis of disease,

and also as a therapeutic. It is useful for screening drugs

effective in the treatment of symptomatic or phenotypic

manifestations perturbing the normal function of MHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

identification of other cellular gene products related to human

kinases, and as reagents in assays for screening compounds that

are useful for treating mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics and pharmacogenomics. Nucleotide construct

cencoding NHP products are used to genetically equineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

cencoding functional NHPs are used in gene therapy for the

modulation of NHP expression.
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     medical
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     biclogical or
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Pred. No. 1.7e-186;
; Mismatches 5;
 compounds useful for treating mental,
                                                                     English.
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Matches
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AAE00491
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(NHP) known as human kinase. The human kinases share structural

similarity with animal kinases, more particularly serine or

threonine protein kinases. Human kinase cDNA is useful for the

detection of mutant human kinase for the diagnosis of disease,

and also as a therapeutic. It is useful for screening drugs

effective in the treatment of symptomatic or phenotypic

manifestations perturbing the normal function of NHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

chantication of other cellular gene products related to human

kinases, and as reagents in assays for screening compounds that

are useful for treating mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics and pharmacogenomics. Nucleotide construct

cencoding NHP products are used to genetically engineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

encoding functional NHPs are used in gene therapy for the

modulation of NHP expression.
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                                                                                                                                                                                                                                                                                                                                   New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases
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6.6e-184;
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Pred. No. 6.6
0; Mismatches
                                                                                                                                                                                                                            Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                               English
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100.0%; Pr
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                                                                                     2000WO-US26621
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342; Conservative
                                                                                                                                                                              GENETICS
                                                                                                                                                                                                                        Turner CA,
                                                                                                                                                                                                                                                                  WPI; 2001-266166/27
N-PSDB; AAD03813,
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WO200123579-AL
                                                                                     27-SEP-2000;
                                                                                                                                 28-SEP-1999;
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"WHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs ceffective in the treatment of symptomatic or phenotypic manifestrations perturbing the normal function of MHP in the body. The MHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human continities and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. WHP oligonucleotides are used as probes. The labelled MHP probactions are used as probes. The labelled MHP probactions and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding functions as bioreactors in the body delivering a continuous supply of MHP to the body. Nucleotide constructs encoding functional MHPs are used in gene therapy for the modulation of MHP expression.
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                                                                                                                                                                                                                         disorder;
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Score 1636; DB 22;
Pred. No. 8.6e-167;
); Mismatches 0;
                                                                                                                                                                                                                          therapy; bioreactor; mental
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Best Local Similarity 90.8%;
Matches 315; Conservative
                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                    2000WO-US26621
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                                                                                                                                                            {first entry}
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08; AADC3817.
                                                                                                                                                                                                                        kinase; gene
cal disorder.
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                                                                                                                                                                                            Humar kinase
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Matches
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                                                                                                                                                                                                                                                                                                                                                Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melancma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic;
SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA
                                                                                                                                    VASOSAGITGKLIPRHOSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLK
                                                                                                                                                -GKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinase polypeptide, useful in diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia
Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Bandman O, Nguyen DB, Lu Y, Burford N, Lal P;
MG, Elliott VS, Recipon SA, Kearney L, Lu DAM;
Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J;
                                                                                                                                                                              347
                                                                                                                                                                                                    315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain"
                                                                                                                                                                             "Eukaryotic protein kinase
                                                                                                  SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIRTL
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4..286
/note= "Eukaryotic |
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                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme
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2000US-222112P.
2000US-222831P.
2000US-224729P.
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                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                             polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                drug screening; transge
hypotensive; anti-HIV;
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Tang
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THORNTON M.
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Patterson C,
Tribouley CM,
Ding L, Yao M
Greenwald SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200208399-A2
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28-JUL-2000;
04-AUG-2000;
                                                                                                                                                                                                                                                                                                                             Human kinase
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The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, laymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addisor's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis), a growth and developmental disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, cardiovascular disorder (e.g., fatty liver, cholestasis, daughertrien), and a lipid disorder (e.g., fatty liver, cholestasis, cardiovascular disorder (e.g., fatty liver, cholestasis), canimals to model humann-plok's disease). PKIN is useful in a number of drug screening techniques and to analyse the protecme of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation cet., among normal, carrier or affected individuals, and as hybridisation in southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (BLISA)-like assays and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The recent
                                                                                                                                                                                                                                                                           inversion,
bridisation
is useful
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growth and developmenta lipid disorder -
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1613; DB 23;
Pred. No. 2.9e-164;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; bloreactor;
        and
                                          Claim 1; Page 147-148; 196pp; English
  ne discrder
disorder and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 324 AA
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  of cancer, immune cardiovascular di
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larity 89.9%;
Conservative
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biological disorder.
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312; Conser
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Best Local S
Matches 312
              sorder
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                                                                                                                                                              AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases
                                                                                                                                                                                                                                                                                                              The present sequence is novel human kinases share structural similarity with animal kinase. The human kinases share structural similarity with animal kinases, more particularly serine or similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the antibodies, as reagents in diagnostic assays, for the can kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonocleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide constructs in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression.
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Pred. No. 3.4e-164;
; Mismatches 0;
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                                                                                                                                                             Friedrich
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Best Local Similarity 90.6%;
Matches 310; Conservative
                                                                                                    99US-0156511
                                                                                                                                                                                                                                                                                             38pp;
                                                                                                                                (LEXI-) LEXICON GENETICS
                                                                                                                                                            Turner CA,
                                                                                                                                                                                                                                                                                            Disclosure, Page 30;
                                                                                                                                                                                      WPI; 2001-266166/27
N-PSDB; AAD03814.
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              WC200123579-A1
                                                                     27-SEP-2000;
                                                                                                  28-SEP-1999;
                                          05-APR-2001
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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and expression and activity. Diseases related to kinase expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers -
                             NCIHRDIKPENILITKGGIIKICDFGFAQIL-------IPGDAYTDYVA
                                                                                                                                                                                                   Human, mouse; protein kinase; antiarthritic; antisclerotic; osteopath; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune discrder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory polvic disease; multiple sclerosis; psoriasis.
                                                                                                                                           RHVDQAGLELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEE
------GKLIPRHQSIFKSNGFFHGISIPEPEDMETLEE
   PNLVNLIEVFRRKRKAMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
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N-PSDB; AAF44670.
                                                                                                                                                                                                                                                                                                                                                           standard;
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QulPL
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AAB65643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU03531-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides or serine/threonine kinase (PTK and STK) families. The polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with imappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. disease), inflammatory disorders (e.g. infertility).

Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays.

The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinases and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding human kinase polypeptides, useful for preventing 1/or treating e.g. cancer, immune, cardiovascular and iated diseases, and microbial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sease;
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4.4e-162;
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Pred. No. 4.
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                                                                                       Protein; 360
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85.2%;
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N-PSDB; AAS06725.
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activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.
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Wehrman
                                                                                          Score 1270.5; CB 2;
Pred. No. 1.5e-127;
); Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide SEQ ID NO 391
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                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                           Guery Match
Best Local Similarity 80.5%;
Matches 243; Conservative
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Liu C,
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N-PSDB; ABQ93433.
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Wang D.
                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                          296 AA;
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The invention relates to an isolated polynucleotide (I) comprising one of administering to a mammalian subject a composition comprising the protein administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II) and (III) are useful for diagnostic evaluation of disorders.
(I), (II) and (III) are useful for diagnostic evaluation of disorders.
(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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               diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder;
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              New polynucleotide and polypeptides, useful for treatment and dof Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, misclerosis, diabetes and allergies -
                                                                                                                                                                                                                                                                                                                                                                          358
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                                                                                     Sequence Listing;
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l Similarity 63.8%;
213; Conservative
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                                                                                                                                                                                                                                                                                                                                              358 AA;
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Matches 213
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The invention relates to an isolated 14257 polypeptide and nucleic acid encoding it. The 14257 protein is a protein kinase that acts as a modulating agent in regulating a variety of cellular processes, including cell proliferation, differentiation, growth and division. The activity of the protein of the invention may be described as; cytostatic; osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive; antiarthritic; dermatological; immunosuppressive; vasotropic; antiatherosclerotic; hypotensive; vasotropic; antiatherosclerotic; hypotensive; vasotropic; antiatherosclerotic; metabolic; immunomodulator and analgesic. The protein of the invention may act as a novel diagnostic target or therapeutic agent controlling certain disorders, for example kinase-associated or other 14257-associated disorders. These may include cellular proliferative disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's disease. Other disorders include bone metabolism disorders such as osteoporosis, disorders of the immune system, e.g. inflammatory, diabetes mellitus, osteoarthritis and asthma. Proteins of
  disorder; hypertension; coronary artery disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New 14257 polypeptides (protein kinases), useful as diagnostic and therapeutic agents for controlling cellular proliferative adifferentiative disorder, bone disorders, immune disorders and cardiovascular disorders
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                                                                      Location/Qualifiers
4..218
/note= "eukaryotic protein kinase domain"
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/note= "serine/threonine protein kinase
signal site"
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serine/threonine-protein ATP-binding
casein alpha chain domain"
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               endothelial cell disorder; psoriasis.
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/note= "c
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  cardiovascular
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  cardiovascular
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the invention may also be of use as therapeutic agents in can
disorders such as hypertension and coronary artery disease, a
endothelial cell disorders, including psoriasis. The current
sequence represents a human kinase 14257 amino acid sequence
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                                                                                                                              MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALR
                                                                                 Length
                                                                                                        Indels
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                                                                               Score 1134; DB 23;
Pred. No. 4.7e-113;
2; Mismatches 2;
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ilarity 98.2%;
Conservative
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N-PSDB; AAF44669.
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complementary sequences may also be used as DNA probes in diagnos assays. The kinase polypeptides may be used as antigens in the prof antibodies of kinase expression and activity. Anti-kinase antiand kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression aractivity include rheumatoid arthritis, atherosclerosis, autoimmudisorders, complications of organ transplantation, myocardial infimune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory belvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, candreproductive disorders.
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                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 16146
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                                                                                                                Score 1123; DB 22;
Pred. No. 8.1e-112;
; Mismatches 0;
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11-JUL-2000;
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                                                                                                                                                                                                                    WIPO
                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                       VASCSAGITGKLIPRHOSIFKSNGFFHGISIPEPEDMETLEEKF---SDVHPVALNFMKG
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53.0%;
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interactions
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ABU11689
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, costeopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipscriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell particularly useful for diagnosing, treating or preventing cell conditions, including adenocarcinoma, disease, acquired immunodeficiency syndrome (ALDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABUI1450-ABUI1845 represent the MDDT polynucleotides encoded by ABUI1450-ABUI1845, described in the disclosure of the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPC at Epperior Specification, thus patent did not form part of the printed specification, thus patent did not form part of the printed specification, but was obtained in electronic format from WIPC at
                                                                                                                                                                                                                     R, Gietzen D, Chinn J;
on O, Yap PE, Amshey SR;
en DA, Kleefeld Y, Gerstin
en AJ, Panzer SR, Harris B
Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                          New purified disease detection and treatment molecule proteins opolynucieotides, useful for diagnosing, treating or preventing (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, oster
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                                                                                                                                                                              Cones AL, Tran AB, Danger, Hillman JL, Yu JY, Tuason SC, Dam TC, Liu TF, Nguyen SC, Dam TC, Liu TF, SA, Chen AM, Lewis SA, Chen
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ilarity 98.9%;
Conservative
            2001US-279619P.
2001US-280067P.
2001US-291280P.
2001US-291829P.
2001US-291849P.
2001US-299428P.
2001US-299428P.
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2001US-299428P.
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N-PSDB; ABX34679.
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180; Conser
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              28-MAR-2001;
29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
20-JUN-2001;
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or hepatitis
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.. 0 180 120 185 65 . O Length 197 Indels Score 948; DB 24; Pred. No. 3.7e-93;); Mismatches 2; 126 99 121 61 9 a ð <u>ය</u> 8

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\$ standard; Protein; AAY90724 RESULT 13
AAY90724
ID AAY90

The present sequence represents a learning-induced kinase, designated KKIAWRE kinase, which is isolated from rabbit brain tissue. KKIAMRE kinase is a cdc2-related kinase. The KKIAMRE kinase polynucleotides can kinase is a cdc2-related kinase. The KKIAMRE kinase polynucleotides can compare brotein for analysis, characterisation or therapeutic use, as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, as chromosome markers or tags, to compare endogenous DNA sequences in patients to identify potential genetic disorders, as probes to hybridise and discover novel related sequences, as a source of PCR primers, and as an antigen to induce anti-DNA antibodies. The polypeptides can be used in assay to discover biological activity, to raise antibodies, as tissue markers, and to isolate correlative receptors or ligands. The polynucleotides may also be used for gene therapy for the treatment of disorders which are mediated by KKIAMRE kinase. memory; detection; earning induced kinase polynucleotides and polypeptides, analysis of learning and memory, and for gene therapy -Rabbit; KKIAMRE kinase; learning-induced kinase; learning; mcdc2-related kinase; brain; gene therapy; genetic disorder; identification. CALLFORNIA Claim 1: Fig 4; 64pp; English 3 П 99WO-US23010 98US-C102906 Sun SEQ entry) KKIAMRE kinase cuniculus SOUTHERN Gomi H, WPI; 2000-328932/28. N-PSDB; AAA29745. (first **\$** Novel learning 999 WC200020567-A2 NIN 02-OCT-1998; 01-OCT-1999; Thompson RF, Oryctolagus 15-AUG-2000 13-AFR-2000 AAY90724; Seguence : ij.e (LYSC-) Rabbit for

47; 566; Length Indels 51.7%; Score 941.5; DB 21; larity 49.7%; Pred. No. 9.7e-92; Conservative 67; Mismatches 65; 67; al Similarity 177; Conserv Ouery Match Best Local (Best Loc Matches

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N-PSDB; AAD03812, AAD03818.
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biological disorder.
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abetes;
disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarction allograft rejection or cancers
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                                                                                                                                                                   Human, protein kinase, enzyme, antiasthmatic, antiinflammatory, antidiabetic; antiparkinsonian; antimigraine; cardiant, cytostatiamunosuppressive, vulnerary, gene therapy, COPD; asthma, migrain chronic obstructive pulmonary disease; non-insulin dependent dial Parkinson's disease; myocardial infarction; inflammatory bowel dautoimmune disorder; allograft rejection; graft versus host diseancer; leukaemia; wound granulation.
             EGRNARRO
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KWNPDDRLTCSQLLESSYF--DSF
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                                                                            standard; Protein;
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06-NOV-2001; 2001US-332870P
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                                                                                                                                              Human protein kinase
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N-PSDB; ABZ77165.
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                                                                   TKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAEL
                                                                                                                                                           New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases
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NMP oligonucleotides are used as probes. The labelled WHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide constructencoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression.
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о ; Length 197; Indels Score 791; DB 22; Pred. No. 2.5e-76; 0; Mismatches C; Query Match Best Local Similarity 100.0%; I Matches 151; Conservative 0;

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is Sequence 11, Application US/09411628
is Patent No. 6428994
is GENERAL INFORMATION:
is APPLICANT: University of Southern California
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
it ITLE OF INVENTION SEQUENCES OF LEARNING-INDUCED KINASES
it ILE REPERBACE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-01
is EARLIER APPLICATION NUMBER: US 60/102,906
is ARLIER APPLICATION NUMBER: US 60/102,906
is ARLIER FILING DATE: 1999-10-02
in CURRENT APPLICATION NUMBER: US 60/102,906
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US-08-93-522-22

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US-08-318-947A-19

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TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES;
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-61
EARLIER APPLICATION NUMBER: US 60/102,906
BARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 493
                 Sequence 4, Application US/09411628
; Fatent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,936
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                                    PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNP-NGVADGVIKSVLWOTLQALNFCHI
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                        MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                       PNLVNLIEVFRRKRKYHLVFEYCOHTLLNELERNPNGVADGVIKSVLWOTLQALNFCHIH
                                                                                    AVASQSAGITGKLIPRHOSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL
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  Gaps
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47;
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Quantitative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
95;
 69;
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Pred. No. 1.1e-50
; Mismatches 99
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 Mismatches
                                                                                                                                                                                                                                                                                                                                   Sequence 113, Application US/09417197; Sequence 113, Application US/09417197; Patent No. 6518021; GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting; TITLE OF INVENTION: On A Cellular Response; FILE REFERENCE: 3759-0110P; CURRENT APPLICATION NUMBER: US/09/417,197; CURRENT FILING DATE: 1999-10-07; CURRENT FILING DATE: 1999-10-07; SEQ ID NOS: 143; SOFTWARE: Patentin version 3.0; SEQ ID NO 113; LENGTH: 544
                                                                                                                                                                                                                                                                                                                                                                                                  Extracting
ar Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: CDK2-EGFP fusion -09-417-197-113
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  68;
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l Similarity 37.2%;
124; Conservative 58
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172;
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ORGANISM: ,
FEATURE:
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Best Local S
Matches 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -AHPFFQ
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-50;
89;
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Pred. No. 1.8e-5
54; Mismatches
                                                                                                                                                                                                                     Edmonds LiP
of the Americas
                                                                                                                                                                               INTERACTIONS
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US/08/969,106
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                                                                                                                                                                                                                                                                                                                                                        2.0
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT THE LESTICE NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 7934 TELEPHONE: 212-790-9090 TELEFAX: 212-869-9741 TELEFAX: 66141 PENNIE
                                                                                                 JS/08969106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Fast SEQ Version 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/96
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
       ...SULT 6
US-09-969-106-2
; Sequence 2, Application US/08
; Patent No. 5986055
; GENERAL INFORMATION:
APPLICANT: Yang, M.
APPLICANT: Yang, M.
APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 INT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmr
STREET: 1155 Aven:
COLVMT
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Best Local Similarity 38.4%;
Matches 118; Conservative (
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino -- ..
                                                                                                                                                                                  ADDRESS:
Pennie & B
1155 Avenue ot
New York
v: USA
0036
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MEDIUM TYPE: Diskett
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TOPOLOGY: unl
OLECULE TYPE:
969-106-2
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COMPUTER:
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US-06-874-347-25

Sequence 25, Application US/C8874347

Patent No. 5863741

GENERAL INFORMATION:

APPLICANT: Limper, Andrew H.

APPLICANT: Leof, Edward B.

APPLICANT: Leof, Edward B.

APPLICANT: Thomas, Charles F.

APPLICANT: Gustafson, Michael P.

TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS

TITLE OF INVENTION: CARINI:

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C., P.A.

STREET: 60 South Sixth Street, Suite 3300

CITY: Minneapolis

STATE: MN

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 298
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1.86-50;
- 89;
288 DVTKPVPHLRLWDPPVATMVSKGEELFTGVVPI 320
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.6%; Score 557; DE
38.4%; Pred. No. 1.86
:ive 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MCLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                              ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
Matches 118; Conser
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Score 557; DB 4; I
Pred. No. 1.8e-50;
I; Mismatches 89;
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                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,125
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
ATTCRNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/COCKET NUMBER: 7934-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                               Edmonds LLP
of the Americas
                                                                                                                                                                                                                                     CDK2 INTERACTIONS
                                                                                                               RESULT 8
US-09-338-125-2
; Sequence 2, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACT:
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmond STREET: 1155 Avenue of the CITY: New York STATE: New York COUNTRY: USA ZIP: 10036 CCMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.4%;
Matches 118; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                              DVTXPVP
                                            GISIPEP
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US-09-338-125-2
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TOPOLOGY: u
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TELEPHONE:
TELEFAX: 2
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                                                                                                              SENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMCCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,522
FILING DATE: 08-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/874,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07039/055002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/874,347
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
                                                                     5-09-093-522-25
Sequence 25, Application US/09093522
Patent No. 6015700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.6%; Scollarity 38.4%; PreConservative 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 67(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
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4: 298 amino acids
amino acid
EDNESS
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CCMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                 294
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Best Local Similarity
Matches 118; Conser
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TOPOLOGY: line
MOLECULE TYPE: I
S-09-093-522-25
            DVTKPVP
                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 60
CITY: Minn
STATE: MN
COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                           - AHPFFC
                                                                                                                                                              PNLVNLIEVFRRKKKMHLVFEYCDHTLLNELERNP-NGVADGVIKSVLWQTLQALNFCHI
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Patent No. 6428994

GENERAL INFORMATION:

APPLICANT: University of Southern California

IITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

CURRENT FILING DATE: 1999-10-01

EARLIER APPLICATION NUMBER: US 60/102,906

EARLIER FILING DATE: 1998-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 298
                                                                                                                                         Indels
                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                    GSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIRTL-
                                                                                                             Score 557; DB 4; I
Pred. No. 4.6e-50;
I; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.5%; Score 556; DB 4; 38.4%; Pred. No. 2.4e-50
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                                                                           EGFP-CDK2 fusion
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OTHER INFORMATION: Xaa
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LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapiens
SOFTWARE: Patentin vers
SEQ ID NO 115
LENGTH: 544
TYPE: PRT
ORGANISM: Artificial S
FEATURE:
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118; Conserv
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NAME/KEY: VARIANT
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US-09-266-225D-14

US-09-266-225D-14

US-09-266-225D-14

Sequence 14, Application US/09266225D

Patent No. 6573364

GENERAL INFORMATION:
APPLICANT: Kingsmore, Stephen
APPLICANT: Tchernev, Velizar

ITTLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak
ITTLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein:
ITTLE OF INVENTION: Interacting Proteins
FILE REFERENCE: 15966-523

CURRENT FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

LENGTH: 298
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Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Informati
TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 298;
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larity 38.4%; Pred. No. 1.8e-50
Conservative 54; Mismatches 8
                --VETGFRHV--
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Best Local Similarity
Matches 118; Conser
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| AVTXPVC
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09-417-197-115
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                                          60 HPNLVNLIEVFRRKRKYHLVFEYCDHTLLNELERNPNG--VADGVIKSVLWQTLQALNFC
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Pred. No. 3.8e-50
3; Mismatches 7.
                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Verenter Application Data:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,620
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                      : Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                  RESULT 13
US-08-461-985-16
Sequence 16, Application US/08461985
Patent No. 5872006
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Yancopoulos, George D.
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of M
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CPERATING SYSTEM: PC-DOS/MS-DOS
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PENNIE
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ilarity 40.5%;
Conservative 58
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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118; Conser
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MOLECULE TYPE:
-08-461-985-16
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STREET: 11
CITY: New
STATE: New
COUNTRY: U
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Matches 118
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PNIVKLLDVIHTENKLYLVFEFTHQDLKKFM5ASALTGIPLPLIKSYLFQLLQGLAFCHS
                                        ---VETGFRHV----DQAGLELLTSS---DPPAVASQSAGITGKLIPRHQSIFKSNGFFH
                              HNCIHRDIKPENILITKOGIJKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQY
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                                                                                 GSSVDIWALGCVFAELLTGOPLWPGKSDVDQLYLIRTL--
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 790-9090
TELEFAX: (212) 869-8864/974:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
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larity 40.5%; Pred. No. 3.8e-50
Conservative 58; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08176620A Patent No. 5595904 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     Boulton, Teri G.
Cobb, Melanie H.
Yancopoulos, George D.
Nye, Steven
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TVPE: amino acids
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APPLICANT: Yancopoulos, (
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, ?
TITLE OF INVENTION: A Far
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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U.S.A.
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Best Local Similarity
Matches 118; Conser
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COMPUTER READABLE
MEDIUM TYPE: F]
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STREET: 11
CITY: New
STATE: New
COUNTRY: U
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GNIVRLHDVIHSEKRIYLVFEYLDLDLKKFMDSCPEFAKNPT---
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Pred. No. 6.9e-50;
68; Mismatches 102;
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DLLSKMLRYEPNKRITARQALEHEYFKDLEMVQ
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     KINASE
                                                Suite
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/C55001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch completed: November 13, 2003, 14:21:59 time : 16.7251 secs
                                                                                                                                                                            J3-JUN-1997
TITLE OF INVENTION: CDC2 PROTEIN K.
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 60 South Sixth Street, St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                <u>о</u>,
                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Vacuarent Application DATA:
APPLICATION NUMBER: US/08/874,3/FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                            26
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Best Local Similarity 34.8%;
Matches 116; Conservative 6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
FENGTH: 294 amino acids
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TOPOLOGY: line
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MOLECULE TYPE: F
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Pred. No. 3.8e-
54; Mismatches
                                                                                                                                                                                                               Patent No. 6387641

GENERAL INFORMATION:
APPLICANT: Vertex Pharmaceuticals Incorporate
APPLICANT: Bellon, Steve
TITLE OF INVENTION: Crystallized P38 Complexe
FILE REFERENCE: VPI/98-14
CURRENT APPLICATION NUMBER: US/09/457,0408
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 29
LENGTH: 298
TYPE: PRT
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US-08-874-347-26
; Sequence 26, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
                                                                                                                                                                                                     Sequence 29, Application US/09457040B
Patent No. 6387641
                                                                                                                                                                                                                                                                                                                                                                                                                      54;
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US-09-457-040B-29
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Best Local S
Matches 118
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Gaps

47;

294;

175

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                 Copyright
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- protein search, using sw model OM protein

November 13, 2063, 14:16:37 Run on:

; Search time 14.6767 Seconds (without alignments) 2273.762 Million cell updates/sec

score: Title: Perfect so Seguence:

US-09-671-050-10 1820 1 MEKYEKLAKTGEGSYGVVFK.....RKARNEGRNRRRQQVLPLKS

347

BLOSUM62 Gapop 10.0 , Sapext 0.5 table: Scoring

283308 segs, 96168682 residues Searched:

283308 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
2: pir2:*
3: pir3:*
4: pir4:* 1 0 E 4

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ription	protein kinase	erine/threonine	rotein kinase (E	rotein kinase (E	rotein kinase (E	rotein kinase (E	rotein Kinase (E	rotein kinase (E	rofein Kinase (B	rotein kinase (B	rotein kinase (E	ELL DIVISION CON	rotein kinase (E	rotein kinase (E	yclin-dependent	rotein kinase (E	rotein kinase ad	rotein kinase (E	rotein kinase (B	rotein kinase (E	otein Kinase (E								
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ALIGNMENTS

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	ies: Homo sapi : 15-Oct-1994 ssion: S23383; rson, M.; Ende : 11, 2909-291 e: A family of rence number: ssion: S23383 us: nucleic ac cule type: mRN dues: 1-358 <m s-references: rfamily: kinas ords: ATP; pho 8/Domain: prot 2/127,129/Acti y Match Local Similar bes 211; Con y Match 127,129/Acti y Match 127,129/Acti 121; Con 121; Con 123; Con 124; Con 125; Con 126; Con 127,129/Acti 127,129/Acti</m
co op op	240 AVASÇSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL 299
6 G	300 KMNPDDRLTCSQLLESSYFDSFQEAQ 325 :

Suery Match Suery Match Sest Local Similarity Set Local Similarity Matches 124; Conservative 66; Mismatches MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKRR MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKRR	protein kinase (EZ 2.7.1.37) cdc2 (similarity) - goldfish C;Species: Carassius auratus (goldfish) C;Species: Carassius auratus (goldfish) C;Accession: ISC474 R;Kajiura, H.; Yamashita, M.; Katsu, Y.; Nagahama, Y. Bev. Growth Differ. 35, 647-654, 1993 A;Title: Isclation and characterization of goldfish cdc2, a catalytic component of matu A;Reference number: ISC474 A;Reference number: ISC474 A;Accession: I	<pre>Query Match Best Local Similarity</pre>
Species: Home procein kinase KKIALRE (EC 2.7.1) - human Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997 Accession: S22745 Mayerson, M.L. Meyerson, M.L. Medetic: 13-76 Amp Medetic: 13-76 Amp Medetics: 1-376 Amp Meyords: 3-136 Meyersonic Specific protein kinase homology Keyords: ATP: phosphotransferase; Serine/threonic-specific protein kinase homology Keyords: ATP: phosphotransferase; Serine/threonic-specific protein kinase homology Keyords: ATP: phosphotransferase; Meyer Match Meyerson: protein kinase homology Keyords: ATP-binding motif Cuery Match Meyerson: Minase ATP-binding motif Meyerson: protein kinase ATP-binding motif Meyerson: protein kinase ATP-binding motif Cuery Match Metches 211; Conservative 41; Mismatches 41; Indels 51; Gaps Matches 211; Conservative 41; Mismatches 51; Gaps Matches 211; Conservative 41; Mismatches 71; [[[[]]]][[[]]][[]][[]][[]][[]][[]][[]]	SSUL	Drotein kinase (EC 2.7.1.37) cdk3 - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: S23382; S22743 R; Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsa R; Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsa R; Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsa R; Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsa R; Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, E.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsa R; Reference number: S23382; MUID:92347325; PMID:1639063 A; Recession: S23382 A; Recession: S23382 A; Residues: U-305 ckEr, A; Residues: U-305 ckEr, A; Residues: 1-305 ckEr, A; Residues: 1-305 ckEr, A; Cross-references: EMBL:X66357; NID:g36612; PIDN:CAA47001.1; PID:g36613 A; Cross-references: GDB:283456 A; Map Dosition: 12q13-12q13 A; Cross-references: GDB:283456 A; Map Dosition: protein kinase homology ckIN, F; 2-255; Domain: protein kinase homology ckIN, F; 10-18/Region: protein kinase ATP-binding motif F; 33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

oocyte

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A,Accession: A37871
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Gross-references: GB:X14227
B,1e Gaellec, R.
submitted to the EMBL Data Library, January 1989
A,Reference number: S15866
A,Accession: M.; Philippe, M.; Le Pennec, J.P.; Lerivray, H.
A,Title: Cloning of the Xenopus laevis cdk2 promoter and functional analysis in ooc
A,Ecross-reference number: I51662; MJD:95129896; PMID:7828909
A,Accession: I51662
A,Accession: I51662
A,Accession: S1662
A,Accession: S1662
A,Accession: MA
A,Residues: L-39 < OLL>
A,Gross-references: EMBL:U07979; NID:9473584; PIDN:AAA82123.1; PID:9473585
C,Genetics:
C,Superfamily: kinase-related transforming protein; protein kinase homology
C,Keywords: ATP; Phosphoprotein; phosphotransferase; serine/threonine-specific prot
C,Genetics:
C,Superfamily: protein kinase ATP-binding motif
F,2-255/Domain: protein kinase ATP-binding motif
F,10-18/Region: protein kinase ATP-binding motif
F,33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
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N;Alternate names: Eg1 homolog; protein kinase p34
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 18-Jun-1999
C;Accession: A41227; S17873; $16520
R;Ninomiya-Tsuji, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K.
Proc. Natl. Acad. Sci. U.S.A. 88, 9006-9010, 1991
A;Title: Cloning of a human cDNA encoding a CDC2-related kinase by complemen A;Reference number: A41227; MUID:92020980; PMID:1717994
A;Accession: A41227
A;Molecule type: mRNA
A;Residues: 1-298 <NIN>
A;Cross-references: GB:M68520; NID:g180177; PIDN:AAA35667.1; PID:g180178
R;Tsai, L.H.; Harlow, E.; Meyerson, M.
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30.5%; Score 555; DB 2; I
Best Local Similarity 37.8%; Pred. No. 5.9e-19;
Matches 115; Conservative 59; Mismatches 90;
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N;Alternate names: cell division control protein CDC2 homolog Eg1
C;Species: Xenopus laevis (African clawed frog)
C;Species: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 18-Jun-1999
C;Accession: A37871; S15866; I51662; S14410
R;Paris, J.; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, F.; Camo, Proc, Natl. Acad. Sci. U.S.A. 88, 1039-1043, 1991
A;Title: Cloning by differential screening of a Xenopus cDNA coding for a p:A;Reference number: A37871; MUID:91126051; PMID:1704128
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$40021
protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostellum protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostellum C.Species: Dictyostellum discoideum S40021; S39071

R.Michaells, C.E.; Weeks, G.
A.Reference mumber: $40021
A.Reference mumber: $40021
A.Reference mumber: $40021
A.Residues: 1-292 cMIC>
A.Reference mumber: BMBL.L00652; NID:g167695; PIDM:AA16056.1; PID:g16
R:Michaells, C.; Weeks, G.
Biochim: Biophys. Acta 1179, 117-124, 1993
A.Reference number: $39071; MUD:94032415; PMID:8218353
A.Reference number: $39071; MUD:94032415; PMID:8218353
A.Residues: 1-18, 'Y. 20-188, 'G', 190-292 cMIZ>
A.Status: preliminary
A.Residues: 1-18, 'Y. 20-188, 'G', 190-292 cMIZ>
A.Status: preliminary
A.Residues: 1-18, 'Y. 20-188, 'G', '190-292 cMIZ>
A.Residues: In Various organisms, cdc2 has been identified as a compone C.Superfamily: kinase-related transforming protein; phosphotransferas F: 2-24/Domain: protein kinase homology cMIN>
F: 10-18/Region: protein kinase ATP-binding motif F: 33, 51, 126, 128/Active site: Lys, Glu, Asp, Lys #status predicted
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12-254/Domain: protein kinase homology <KIN>
110-18/Region: protein kinase ATP-binding motif
133,51,126,128/Active site: Lys, Glu, Asp, Lys #status predicted
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35.0%; Pred. No. 4e-19;
ive 66; Mismatches 101;
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Notiternate names: GEC 2.7.1.37) cdc2 - Arabidopsis thailana
Notiternate names: cdc2 protein homolog; CCC2a protein; cell division control pro
C, Species: Arabidopsis thailana (mouse-ear cross)
C, Date: 22-Nov-1993 #sequence_revision 03.Nov-1995 #text_change 20-Jun-2000
C, Accession: S204 79.77, 1992
Filaliku, Y; Hirayama T; Endoh, H; Oka,
A; Title: Exon-intron organization of the Arabidopsis thaliana protein kinase gene
A; Title: Exon-intron organization of the Arabidopsis thaliana protein kinase gene
A; McCession: S23095
A; McCession: McC
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              protein
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                                                                                                                     Score 552.5; DB 2;
Pred. No. 7.5e-19;
5; Mismatches 98;
            transforming protein;
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        C;Superfamily: kinase-related transforming protes
C;Keywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys
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B40444
protein kinase (EC 2.7.1.37) cdc2 homolog B - maize (fragme c.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_cfC; Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_cfC; Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_cfC; Date: 14-Feb-1992 #text_cfC; Date: 1501ation and characterization of cDNA clones encomplete: 1501ation and characterization of cDNA clones encompletes: 1501ation and characterization of cDNA clones encompletes: 1501ation and characterization of cDNA clones encompletes: 1501ation and characterization of cDNA clones A; Reference number: A40444
A; Reference number: A40444
A; Residues: 1-294 <COL>
A; Residues: 1-294 <COL>
A; Cross-references: GB:M60526
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Pred. No. 6.5e-19;
54; Mismatches 89;
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61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQAL 11	SULT 11 SULT 11 SULT 11 SULT 11 Species: Zea mays (maize) Accession: A40444 Colasanti, J.; Tyers, M.; Sundaresan, V. Oct. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991	tle: Isolation and characterization of cDNA ference number: A40444; MUID: 91195354; PMID cession: A40444 MUID: 91195354; PMID cession: A40444 at us: preliminary lecule type: mRNA sidues: 1-294 <col/> OSS-references: GB:M60526 perfamily: kinase-related transforming protywords: ATP; phosphotransferase 256/Dcmain: protein kinase homology <kin>-18/Region: protein kinase ATP-binding moti ,51,127,129/Active site: Lys, Glu, Asp, Lys</kin>	30.0%; Score 546.5; DB 1; Length 294; conservative 66; Mismatches 93; Indels 67; Gaps KYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLK	116 AYCHSHRULHDERFINALKLADFGLARAFGIPVRTFTHEVVTLWYRAPEIL 175 173 VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDGLYLIRTLVETGFRHVDQAGLEL 232 174 LGARQYSTPVDWWSVGCIFAEMVNQKPLFPGDSEIDELFKIFRILG
A;Molecule type: mRNA A;Residues: 1-294 «FER» A;Residues: 1-294 «FER» A;Cross-references: GB:S45387; NID:g257373; PIDN:AAB23643.1; PID:g257374 A;Experimental scurce: flower C;Comment: The protein is a key component of the eukaryotic cell cycle. C;Genetics: A;Gene: cdc2 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3 C;Function: A;Gene: cdc2 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3 C;Function: A;Gene: cdc2 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3 C;Function: A;Gene: cdc2 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3 C;Function: A;Gene: cdc2 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3 C;Function: A;Gene: cdc2 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3 C;Function: A;Gene: cdc2 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3 C;Function: Phosphotransferase; required for G; to S-phase transition C;Guperfamily: kinase-related transforming protein, protein kinase homology «KIN» F;2-256/Domain: protein kinase ATP-binding motif F;30-18/Region: protein kinase ATP-binding motif F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted	30.3%; Score 551.5; DB 2; Length 294; 11 Similarity 35.5%; Pred. No. 8.4e-19; 11 Similarity 35.5%; Pred. No. 8.4e-19; 11 Similarity 35.5%; Pred. No. 8.4e-19; 11 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKPRRITE	178 YGSSVDIWAIGCVFAELLTGCPLWPGKSDVDQLYLIIRTLVETGFRHV : : :	SULT 10 2440 otein kinase (EC 2.7.1.37) cdc2 homolog Species: Oryza sativa (rice) Date: 13-Jan-1995 #sequence_revision 13 Accession: S22446 Hashimoto, J.; Hirabayashi, T.; Hayano, 1. Gen. Genet. 233, 10-16, 1992 Title: Isolation and characterization of Reference number: S22440; MJID:92293101 Accession: S22440	Molecule type: Residues: 1-29 Cross-referency Superfamily: k Keywords: ATP; 2-256/Domain: ;2-256/Domain: ;33,51,127,129/ Query Match Best Local Sim Matches 116; Y IME

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Gaps

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protein kinase (EC 2.7.1.37) cdk2 [validated] - goldfish C.Species: Carassius auratus (goldfish) - goldfish C.Species: Carassius auratus (goldfish) - G.Species: Salay-2000 - G.Accesion: A44878 - G.Species: Salation and characterization of goldfish cdk2, a cognate variant of the cel A; Reference number: A44878 - MUID:9231802; PMID:1339336 - Gognate variant of the cel A; Reference number: A44878 - G.Species: 1-298 - G.Species: G.Species:
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                                                                                                             Score 545; DB 2; L
Pred. No. 1.7e-18;
; Mismatches 74;
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Pred. No. 1.7e-18;
8; Mismatches 67;
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Best Local Similarity 46.6%;
Matches 102; Conservative 4
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Best Local Similarity 40.2%;
Matches 117; Conservative
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photransferase;
T49271
CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A - Arabidopsis thaliana
N;Alternate names: protein T21318.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2006 #text_change 59-Jun-2000
C;Accession: T49271
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.;
Submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25021
A;Accession: T49271
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A;Cession: T49271
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A;Cession: Gabel: C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.;
A;Cession: T49271
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Cyclin-dependent kinase 1 - bovine
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CyAccession: 145977
R:Yang, L.; Farin, C.E.
Gene 141, 281-286, 1994
A;Title: Identification of cDNAs encoding bovine cyclin B and Cdki/Cdc2.
A;Reference number: 145977; WUID:94215918; PMID:8163203
A;Accession: 145977; WUID:94215918; PMID:8163203
A;Accession: 145977; WID:94215918; PMID:8163203
A;Accession: 1297 < YAN>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: GB:L26547; NID:9433155; PIDN:AAA18894.1; PID:9498173
C;Genetics:
A;Gene: cdk1/cdc2
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;2-256/Domain: protein kinase homology <KIN>
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**REGULATE OF 339-789 FROM N.A.

**Andreesen J.D.;

**Andreesen J.D.;

**Andreesen J.D.;

**Differential screening leads to novel genetic markers of monocyte

**To macrophage maturation.";

**Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.

**CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

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MODLINE=98389628; PubMed=9721213;
Montini E., Andolfi G., Caruso A., Buchner G., Walpole S.M.,
Mariani M., Consalez G.G., Trump D., Ballabio A., Franco B.;
"Identification and characterization of a novel serine-threonine kinase gene from the Xp22 region.";
Genomics 51:427-433(1998).
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                   Score 1157.5; DB Pred. No. 9.8e-75; Hismatches 43
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GK, O76039; ---

R MIM; 300203; ---

R GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.

R GO; GO:0005468; P:protein amino acid phosphorylation; TAS.

R GO; GO:0005468; P:protein amino acid phosphorylation; TAS.

R GO; GO:0006468; P:protein amino acid phosphorylation; PROTEIN KINASE ATP; 1.

R PROSITE; PSC0109; PROTEIN KINASE ATP; 1.

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                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM TISSUE=Cocyte
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GO; GO: 00.

GO; GO: 0000074.

InterPro; IPR002290; Ser.

R Ptam; PF00369; pkinase; I.

DR SMART; SM0220; STKG: I.

DR PROSITE; PSC0100; PROTEIN KINASE ATP; I.

DR PROSITE; PSC0110; PROTEIN KINASE ATP; I.

DR PROSITE; PSC0111; PROTEIN KINASE ATP; I.

TOMAIN

TO 10 18 ATP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

TO 127 BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

TO 127 BY SIMILARITY).

TO 128 BECOSÉA262A CRC64;

TABLE BECOSÉA262A CRC64;

TABLE BECOSÉA262A CRC64;

TABLE BECOSÉA262A CRC64;

TABLE BECOSÉA26A CRC64;

TABLE BECOSÉA CRC64;

TABLE BECOSÉA
                                                                                                                                                                                                                                                                                                                                              CELL CYCLE.
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                                                                           Eutelecstomi
Homo.
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                                                                           Craniata, Vertebrata, ?
Catarrhini, Hominidae,
                                                                                                                                                                                                                                                     1.-K., Gorka
                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE=Fetal brain;

MEDLINE=92347325; PubMed=1639063;

Meyerson M., Enders G.H., Wu C.-L., Su L.-K., Gork

Harlow E., Tsai L.-H.;

"A family of human cdc2-related protein kinases.";

EMBO J. 11:2909-2917(1992).

-!- FUNCTION: PROBABLY INVCLVED IN THE CONTROL OF

INTERACTS WITH A YET UNKNOWN TYPE OF CYCLIN. C
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                                                                                                                                                                                                                                                                                                                                                                                                                        THE SER/THR FAMILY
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MIM; 123828; -.

GO; GO:0004693; F:cyclin-dependent prot
GO; GO:0007048; P:oncogenesis; TAS.
GO; GO:000074; P:regulation of cell cy
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
     2.7
    m
                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
     kinase
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PIR; S23382; S23382.
PDB; 1LFN; 24-APR-02.
Genew; HGNC:1772; CDK3.
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELCNGS CDC2/CDKX SUBFAMILY
     protein
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  division
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SEMBL, D1758; BAA04605.1; -.

DR PIR; 150474; 150474.

BRS: 700514; 1B18.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR00001; Prot kinase, 1.

DR PROSITE; PR00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PR00107; PROTEIN KINASE ET; 1.

Transferace; Serine/threonine-protein kinase; ATP-binding;

Transferace; Serine/threonine-protein kinase; ATP-binding;

TRANSTERM KINASE

4 18 ATP (BY SIMILARITY).

TY SIMILARITY.
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219
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ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES SIMILARITY).
                                                       SDPPAVASOSA - - GITGKLIPRHQSIFKSNGFFHGISIPEPE-DMETLEEKFSDVHPVAL
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-PKWTRKGLEEIVPNLEPEGR
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; Cypriniformes
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"Isolation and characterization of goldfish cdc2, a catalytic component of maturation-promoting factor.";
Dev. Growth Differ. 35:647-654(1993).
-! - FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC C CYCLE. IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO S-PHASE MITOSIS. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II. CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: FORMS A STABLE BUT NON-COVALENT COMPLEX WITH CYCLIN MATURE OOCYTES.
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CDC2/CDKX SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprini
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
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Pipidae;
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                                                                                          Shuttlewor
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MEDLINE=93345457; PubMed=8393783;
Poon R.Y.C., Yamashita K., Adamczewski J.P., Hunt T., Shuttlew Poon R.Y.C., Yamashita K., Adamczewski J.P., Hunt T., Shuttlew Poon R.Y.C., Yamashita K., Adamczewski J.P., Hunt T., Shuttlew Poon R.Y.C., Yamashita K., Adamczewski J.P., Hunt T., Shuttlew Foon R.Y.C., Yamashita I., Adamczewski J.P., Hunt T., Shuttlew Foon R.Y.C., Protein Kinase that can activate p33cdk2 and p34cdc2.";
EMBO J. 12:3123-3132(1993).
-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYC INTERACTS WITH CYCLINS A, D, CR E.
-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INA THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT SIMILARITY).
-!- DEVELOPMENTAL STAGE: SYNTHESIZED IN UNFERTILIZED EGG, BUT
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                             CRC64;
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROT
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.a; Pipcidea;
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TISSUE=Ovary;

MEDLINE=91126051; PubMed=1704128;

Paris J., le Guellec R., Couturier A., le Guellec Camonis J., Macneill S., Philippe M.;

"Cloning by differential screening of a Xenopus protein highly homologous to cdc2.";

Proc. Natl. Acad. Sci. U.S.A. 88:1039-1043(1991)
                                                         3;
71;
PHOSPHORYLATION (3Y PHOSPHCRYLATION (3Y PHOSPHCRYLATION (BY ), 58D3812E19B311F5 (
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Last sequence update;
Last annotation update;
kinase 2 (EC 2.7.1.-)
                                               Score 563; DB
Pred. No. 6.9e-0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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  restrictions on
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                                                                                        EMBL, X14227; CAA32443.1; -..

PIR; A37871; A37871.

HSSP; F24941; 1BUH.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR002290; Ser_thr_pkinase.

Probom; PD000001; Prot_kinase; 1.

Probom; PD000001; Prot_kinase; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN KINASE_BOM; 1.

PROSITE; PS0011; PROTEIN KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN KINASE_TY 1.

PROSITE; PS0011; PROTEIN KINASE.

ATP (BY SIMILARITY).

ACT SITE 127 127 BY SIMILARITY).

MCD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).

MCD_RES 15 15 PHOSPHORYLATION (BY CAK).

SEQUENCE 297 AA; 33969 MK; EC30204FCBBD198C CRC64;
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AC P34117;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1999 (Rel. 28, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT CDC2-like serine/threonine-protein kinase CRP (ECGN CRPA OR CRP.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostel:
OX NCBI_TaxID=44689;
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                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Frobom; PF00069; pkinase; 1.
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ProDom; PF001001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
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Transferase; Serine/threonine-protein kinase; Phosphorylation.
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Biochim. Biophys. Acta 1179:117-124(1993).

-!- ENZYME REGULATION: PHOSPHORYLATION AT TH
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-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY.

CDC2/CDKX SUBFAMILY.
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Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung Midder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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11 cycle regulation of CDK2 activity by phosphorylation of
Tyr15.";
) J. 11:3995-4005(1992).
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"Cloning of a human cDNA encoding a CDC2-related kinase by
complementation of a budding yeast cdc28 mutation.";
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Catarrhini; Hominidae; Homo
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MEDLINE=93288132; PubMed=8510751;
de Bondt H.L., Rosenblatt J., Jancarik
Morgan D.O., Kim S.-H.;
"Crystal structure of cyclin-dependent
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MEDLINE=93010995; Pubmed=1396589
Gu Y., Rosenblatt J., O'Morgan D
                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A. MEDLINE=91367262; PubMed=1653904
                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBL_TaxID=9606;
01-AUG-1992 (Rel. 23,
15-SEP-2003 (Rel. 42,
Cell division protein
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SEQUENCE FROM N.A.
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X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITG CKS1.
MEDLINE=96182647; PubMed=8601310;
Bourne Y., Watson M.H., Hickey M.J., Holmes W., Rocque W., Reed S.I.
Tainer J.A.;
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MEDLINE=97475219; PubMed=9334743;
Lawrie A.M., Noble M.E.M., Tunnah P., Brown N.R., Johnson L.N.,
                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.33 ANGSTROMS) OF COMPLEX WITH L868276. MEDLINE=96181476; PubMed=8610113; de Azevedo W.F. Jr., Muleer-Dieckmann H.-J., Schulze-Gahmen U., Worland P.J., Sausville E., Kim S.-H.; Worland P.J., Sausville E., Kim S.-H.; "Structural basis for specificity and potency of a flavonoid inhibitor of human CDK2, a cell cycle kinase."; Proc. Nati. Acad. Sci. U.S.A. 93:2735-2740(1996).
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                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH MEDLINE=95356811; PubMed=7630397; Jeffrey P.D., Russo A.A., Polyak K., Gibbs E., Hurwitz Massague J., Pavletich N.P.; "Mechanism of CDK activation revealed by the structure cyclinA-CDK2 complex."; Nature 376:313-320(1995).
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MEDLINE=98342369; PubMed=9677190;
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Kim S.H., Lockhart D.J., Schultz P.G.;
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-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF
INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF
DURING S PHASE AND G2.
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PDB; 1HCK; 07-DEC-96.
PDB; 1HCK; 07-DEC-98.
PDB; 1HCK; 07-DEC-98.
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PDB; 1B101; 29-JUL-97.
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PDB; 1H10; 19-SEP-02.
PDB; 1H20; 19-SEP-02.
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THE CONTROL OF THE CELL CYCLE.

RE. ACTIVITY OF CDK2 IS MAXIMAL

ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACT THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES CDC2/CDKX SUBFAMILY.

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Local Similarity 34.8
es 116, Conservative
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SEQUENCE FROM N.A.

STRAIN=cv. Nipponbare;

MEDLINE=92293101; PubMed=1376401;

Hashimoto J., Hirabayashi T., Hayano Y., Hata S., Ohashi Y.,

A suzuka I., Utsugi T., Toh-E A., Kikuchi Y.;

Lisolation and characterization of cDNA clones encoding cdc2

Thomologues from Oryza sativa: a functional homologue and cognate

Thomologues from Oryza sativa: a functional homologue and cognate

Total Gen. Genet. 233:10-16(1992).

Mol. Gen. Genet. 233:10-16(1992).

Mol. Gen. ComPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES

THE REPETITIVE CARBOXLL-TERMINUS OF RNA POLYMERASE II.

THE REPETITIVE CARBOXLL-TERMINUS OF RNA POLYMERASE II.

THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY

SIMILARITY).

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

COC2/CDKX SUBFAMILY.
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PIR; S22440; S22443.

HSSP; P24941; IHCL.

Gramene; P29618; -.

InterPro; IPR000719; Prot kinase.

InterPro; IPR00250; Ser thr pkinase.

InterPro; IPR002290; Ser thr pkinase.

Prodom; PD00069; pkinase; I.

ProDom; PD00069; pkinase; I.

PROSITE; PS00109; PROTEIN KINASE ATP; I.

PROSITE; PS001108; PROTEIN KINASE DOM; I.

PROSITE; PS00111; PROTEIN KINASE DOM; I.

Transferase; Serine/threonine-protein kinase; ATP-binding;

Cell cycle; Cell division; Mitosis; Phosphorylation.

DOMAIN 4 287 PROTEIN KINASE.
                                                                                                                                                                               CDC2-1.

Oryza sativa (Rice).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracho Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Cryza.

NCBI_TaxID=4530;
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01-APR-1993
01-CCT-1996
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CC2A ARATH

CC2A ARATH

CC2A ARATH

P24100; Q9M307;

C1-MAR-1992 (Rel. 21, Created)

C1-MAR-1992 (Rel. 41, Last sequence update)

C1-MAR-1992 (Rel. 41, Last annotation update)

28-FEB-2003 (Rel. 41, Last annotation update)

Cell division control protein 2 homolog A (EC 2.7.1.-).

CDC2A OR CDC2 OR AT3G48750 OR T21J18 20.

Arabidopsis thaliana (Mouse-ear cress),

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Spermatophyta; Massicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
MEDLINE=92316202; PubMed=1618302;
Imajuku Y., Hirayama T., Endoh H., Oka A.;
"Exon-intron organization of the Arabidopsis thaliana protein kinase
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MEDLINE=92039027; PubMed=1937013;
Hirayama T., Imajuku Y., Anai T., Matsui M., Oka A.;
Hidentification of two cell-cycle-controlling cdc2 garabidopsis thaliana.";
Arabidopsis thaliana.";
Gene 105:159-165(1991).
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Pred, No. 4.3e-32;
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MEDLINE=93005715; PubMed=1840925;
Ferreira P.C.G., Hemerly A.S., Villarroel
"The Arabidopsis functional homolog of the Plant Cell 3:531-540(1991).
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SEQUENCE FROM N.A.
MEDLINE=92339744; PubMed=1634002;
Inze D., Ferreira P.C.G., Hemerly A.S.,
"Control of cell division in plants.";
"Control of rans. 20:80-84(1992).
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MEDLINE=21016720; PubMed=11130713
                    68;
   34.8%;
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ett. 304:73-77(1992)
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As Salamoubat M., Lemcke K., R.eger M., Ansorge W., Unseid N..

As Partmann B., Valle G., Blocker H., Perza Alonza M., Cobrasier B.,

As Partmann B., Valle G., Blocker H., Perza Alonza M., Cobrasier B.,

As Cosmon V., Choise N. Matiguerave F., Robert C., Brotter P.,

As Graded M. Maller-Auer S., Cabel C., Enchs M., Bersa V.,

R. Marchann R., Kranz H., Volovi H., Malland R., Bandt P., Nyakatura G.,

R. Marchann R., Kranz H., Volovi H., Holland R., Bandt P., Nyakatura G.,

R. Marchann R., Kranz H., Volovi H., Holland R., Bandt P., Nyakatura G.,

R. Marchann R., Kranz H., Polovi H., Holland R., Bandt P., Nyakatura G.,

R. Coske R., Laudiac C., Relaza G., Lochmer T., Nordale G.,

R. Marro P., Collado C., Berza-Perza A., Otterwaelder B., Duchemin D.,

R. Marro P., Collado C., Berza-Perza A., Otterwaelder B., Duchemin D.,

R. Marro P., Collado C., Berza-Perza A., Otterwaelder B., Duchemin D.,

R. Mannhaupt G., Haase D., Schoof H., Tallon L.C., Seacuberta E.,

Mannhaupt G., Haase D., Sallers M., Lignor R., Visale D.,

R. Mayer R. R. X. Kann C. D., Koo H., Tallon L.C., Shar T.P.,

R. Rocker A., Majirato A., Flores M., Lignor R., Wisale D.,

R. Mannhaupt G., Mallers B., Malti R., Wu D., Peterson J., Van Aken S.,

R. Rocker D., Lin X., Marman W. C., Salberg S.L., White O., Venter J., C.,

R. Mannhaupt G., Marko M., Marmunc O., Koo H., Tallida Y.,

R. Kannza E., Marman M., Nakmunca Y., Sato S., Kato T., Asabita E.,

R. Kannza E., Marman M., Marbunct O., Mursa J., Van Asabita E.,

R. Kannza E., Marman M., Marbunct O., The Eldhida Y.,

R. Kannza E., Marman M., Marbunct O., Mursa J., Van Asabita E.,

R. Kannza E., Marman M., Marbunct O., The Barda T.,

R. Mayama S., Marzaki M., Shingo S., Rato C., White O., Venter J. C.,

R. Kannza E., Marman M., Marbunct O., The Eldhida Y.,

R. Sasorto S., Kimiz T., Ideawa X., Kaushima K., Kaushima M.,

R. Sasorto S., Kimiz T., Ideawa X., Kaushima M., Thada T.,

R. Racker R. Edularia M., Shingo S., Rato C., White J.,

R. Sasorto S., Kimiz T., Marman M., Marbunct O., Wurter J., Markayama S.,
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cycle EMBL; S45387; AAB23643.1; -..

EMBL; M59198; AAA32831.1; -..

EMBL; M59198; AAA32831.1; -..

EMBL; M59198; AAA32831.1; -..

EMBL; X57839; CAA43971.1; -..

EMBL; X57839; CAB47971.1; -..

EMBL; X53095; S23095.

PIR; S23095; S23095.

RESP, P24941; 1HCL.

RICE PROOF P24941; 1HCL.

InterPro; 1PR000719; Prot kinase.

InterPro; 1PR0002290; Ser thr pkinase.

RESP, P24941; 1HCL.

InterPro; 1PR0002290; Ser thr pkinase.

RESP, P24941; 1HCL.

REMBL; P240910; PROTEIN KINASE ATP, 1HCL.

REMBL; P240910; PROTEIN KINASE DOM; 1HCL.

REMBL; P240910; PA40910; PROTEIN KINASE DOM; 1HCL.

REMBL; P240910; PA40910; PA4091 PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY CAK) (BY SIMILA
B5FAE55FA9EC366E CRC64; ; Phosphorylation. PROTEIN KINASE. ATP (BY SIMILARITY) ATP (BY SIMILARITY) 34030 MW; 18 33 127 14 15 sion; Mitosis 4 287 294 AA; 10 33 127 14 14 15 NP BIND BINDING ACT SITE MOD_RES MOD_RES SEQUENCE Cell

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MAXIMAL
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ENA Cell Biol. 20:413-423(2001).

-:- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE. INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMA DURING S PHASE AND G2.
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551.5; DB 1,
NO. 4.3e-32;
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SIMILARITY: BELONGS TO THE SER/THR FAMILY
CDC2/CDKX SUBFAMILY.
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IsoId=O55076-1; Sequence=Displayed;
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Eukaryota, Metazoa,
Mammalia, Eutheria,
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Matches 115
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C Q9DGA2; Q9DGA1;

C Q9DGA2; Q9DGA1;

T 28-FEB-2003 (Rel. 41, Last annotation update)

T 28-FEB-2003 (Rel. 41, Last annotation update)

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R HSSP; P24941; 1AQ1.

R InterPro; IPR002719; Prot kinase.

R InterPro; IPR00229C; Ser thr_pkinase.

R InterPro; IPR00229C; Ser thr_pkinase.

R Prodom; PD0000001; Prot kinase; 1.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC CONTROL: IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO S-PHASE PRIOSIS. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II. CATALYTIC COMPONENT OF MPF (By similarity).

ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY
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SUBUNIT: FORMS A STABLE BUT NON-MATURE COCYTES (By similarity).

SUBCELLULAR LOCATION: Nuclear (By SIMILARITY: BELONGS TO THE SER/T CDC2/CDXX SUBFAMILY.
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R fam; PF00069; pkinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R PROSITE; PS00108; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS50011; PROTEIN KINASE DOM; 1.

R PROSITE; PS50011; PROTEIN KINASE DOM; 1.

R Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cy Cell division; Mitosis; Phosphorylation; Alternative splicing.

4 286 PROTEIN KINASE.

4 A 286 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INACTI
IT (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYCLE
                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rai
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                   a maligna
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SEQUENCE OF 19-124 FROM N.A.

SEQUENCE OF 19-124 FROM N.A.

MEDLINE=96113578; PubMed=8673024;

A Hosokawa Y., Yang M., Kaneko S., Tanaka M., Nakashima K.;

Hosokawa Y., Yang M., Kaneko S., Tanaka M., Nakashima K.;

T Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F-T

T during the prolactin-induced G1/S transition in rat Nb2 pre-T

T during the prolactin-induced G1/S transition in rat Nb2 pre-T

T during the prolactin-induced G1/S transition in rat Nb2 pre-T

T during the prolactin-induced G1/S transition in rat Nb2 pre-T

T during the prolactin-induced G1/S transition in rat Nb2 pre-T

T During the prolactin-induced G1/S transition in rat Nb2 pre-T

SC -!- FUCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYC

INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAX

DURING S PHASE AND G2.

-!- FUZYME REGULATION: PHOSPHORYLATION AT THR-160 ACTIVATES IT

SIMILARITY).

SIMILARITY).

SIMILARITY).

**THEDMATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                       Cdk2) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).

!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
    Name=CDK2-alpha;
    IsoId=Q63699-1; Sequence=Displayed;
    Name=CDK2-beta;
    IsoId=Q63699-2; Sequence=Not described;
    IsoId=Q63699-2; Sequence=Not described;
    IsoId=Q63699-2; Sequence=Not described;
    CDC2/CDKX SUBFAMILY.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUE=Thyroid;

MEDLINE=95166553; PubMed=7862443;

Kotani S., Endo T., Kitagawa M., Higashi H., C;

Kotani S., Endo T., Kitagawa M., Higashi H., C;

"A variant form of cyclin-dependent kinase 2 {

transformed rat thyroid (FRTL-TC) cell line.";

Oncogene 10:663-669(1995).
                                    ALNFMKGCLKYNPDDRLTCSQLLESSYFDSFQEAQI
                                                                                                                                063699; 009136;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cell division protein kinase 2 (EC 2.7.1.-).
                                                                                                                       298
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EMBL; D63162; BAA09638.1; -.
HSSP; P24941; 1AQ1.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase
Pfam; PF00069; pkinase; 1.
                                                                                                                    STANDARD;
                  291
                                              260
                                                                                                       K2_RAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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SIMILARITY).
CAK) (BY SIMILARITY)
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Cricetinae;
                                                                                                                                                   46;
                                                                                                                          Length 298
                                                                                                                                                   Indels
                                                                                                    CRC64;
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ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (BY PHOSPHORYLATION (BY V -> C (IN REF. 2).

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L -> C (IN REF. 2).

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89;
    LARITY)
                                                                                                                           core 548; DB 1;
red. No. 7.8e-32
Mismatches 8
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Last annotation update
kinase 2 (EC 2.7.1.-)
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Mesocricetus auratus (Golden hamster).

Eukaryota; Metazoa; Chordata; Craniata; Ver
Mesocricetus.

Mesocricetus.

NCBI_TaxID=10036.
                                                                                                                            Score 548;
Pred. No.
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33
127
14
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124
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133887 MW;
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01-FEB-1996 (Rel. 33, Last seq
15-JUL-1999 (Rel. 38, Last ann
Cell division protein kinase 2
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imilarity 38.1%;
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Best Local Si
Matches 117;
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    entities ...

or send an email ...

send an email ...

RBBL; D17350; BA204165.1; -..

RBSL; D17350; BA204165.1; -..

R InterPro; IPR002290; Ser_th_pkinase.

R InterPro; IPR002290; Ser_th_pkinase.

R InterPro; IPR002290; Ser_th_pkinase.

DR Prosite; PS00107; Protein Kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00109; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00109; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00109; PROTEIN KINASE DOM; 1.

Transferase; Serine/thronine-protein kinase; ATP-binding;

KW Cell cycle; Cell division; Mitosis; Phosphorylation.

Transferase; Serine/thronine-protein kinase; ATP-binding;

FT NP BIND 4 286

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

Thomas ATP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

Thomas ATP (BY SIMILARITY).

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Thomas ATP (BY 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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   Usage
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                                                                                                                                                                                                                                                                                                                                                Score 546; DB 1; 1
Pred. No. 1.1e-31;
54; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDC2 HUMAN PC64; PC6493; O60764; PC6493; O60764; O1-JAN-1988 (Rel. 06, Last sequence update); O1-JAN-1988 (Rel. 42, Last annotation update); I5-SEP-2003 (Rel. 42, Last annotation update); Cell division control protein 2 homolog (EC 2.7 Cell division dependent kinase 1) (CDK1).
and this statement is not removed. requires a license agreement (See in email to license@isb-sib.ch).
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ilarity 38.1%;
Conservative 54
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MEDLINE=87201915; PubMed=3:
Lee M.G., Nurse P.;
"Complementation used to c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - VETGFRHV
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Best Local Similarity
Matches 117; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skin;

XEDINE-22388257; PubMed=12477932;

XEDINE-22388257; PubMed=12477932;

XITAUSDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soaree M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wckernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYMERASE II.

ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT.

SUBUNIT: FORMS A STABLE BUT NON-COVALENT COMPLEX WITH A REGULATORY SUBUNIT AND WITH A CYCLIN.

SUBCELLULAR LOCATION: Nuclear (By similarity).

POLYMORPHISM: Isoform CDC2deltaT is found in breast cancer tissues. It is unable to complex with cyclin B1 and also fails to bind to the CDK inhibitor p21.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                          s eliminates binding p21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHÓSPHORYLATION, AND ASSOCIATION WITH P13.

MEDLINE=88253421; PubMed=3289755;

Draetta G., Beach D.;

"Activation of cdc2 protein kinase during mitosis in human cells:
cell cycle-dependent phosphorylation and subunit rearrangement.";

Cell 54:17-26(1988).

-!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC

CELL CYCLE. IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO S-PHASE
AND MITOSIS. P34 IS A COMPONENT OF THE KINASE COMPLEX THAT

PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA
                                                                                                                                                                                                                                                 Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 Fukuda M.,
                                                                                                                                                                                                                                                                                                                "T-loop deletion of CDC2 from breast cancer tissues
to cyclin B1 and cyclin-dependent kinase inhibitor g
Cancer Res. 58:1095-1098(1998).
                                                                                                                                                                                                                                               χ.,
                                                                                                                       AND VARIANT CDC2DELTAT
                                                                                                                                                                                                                                                 Shibata
                                                                                                                                                                                                    PubMed=9515786;
., Isohashi F.,
cycle control gene cdc2."; re 327:31-35(1987).
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                                                                                                                                                              TISSUE=Breast cancer;
MEDLINE=98175539; Pub
Ohta T., Okamoto K.,
                                   Nature 327:31-35(196
[2]
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/*FId=VAR_011629.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; 3
Actinopterygii; Neopterygii; Teleostei; Ostariophysi Cyprinidae; Carassius.
NCBI_TaxID=7957;
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ed. No. 1.3e-31;
Mismatches 74;
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(Rel. 38, Last annotation update
EMBL; Y30272; CAA68375.1; -.

EMBL; D88357; BAA26001.1; -.

EMBL; AF512554; AAM34793.1; -.

EMBL; AR59539; A29539.

PDR; 1LC9; 17-APR-02.

SWISS-2DPAGE; P06493; HUMAN.

Genew; HGNC:1722; CDC2.

GK; P06493; -.

GN; P06669; PROCE kinase.

InterPro; IPRC02290; Ser thr pkinase.

ProDom; PD000001; Prot kinase; 1.

PROSITE; PSC0107; PROTEIN KINASE ATP; 1.

PROSITE; PSC0108; PROTEIN KINASE DOM; 1.

PROSITE; PSC0108; PROTEIN KINASE DOM; 1.

PROSITE; PSC011; PROTEIN KINASE DOM; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R FIR; A44878; A44878.

R HSSP; P24941; 1FIN.

R HSSP; P24941; 1FIN.

R HSCP; P24941; 1FIN.

R PRO02290; Ser thr pkinase.

R Proncion; Proficion; Kinase.

R PROSITE; PSC0109; PROTEIN KINASE ATP; 1.

R PROSITE; PSC0107; PROTEIN KINASE DOM; 1.

R PROSITE; PSC0101; PROTEIN KINASE DOM; 1.

R PROSITE DOM; 1.

R PROSITE DOM; PROSITE DOM; 1.

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                                                                                                      Hirai T., Yamashita M., Yoshikuni M., Tokumoto T., I
Sakai N., Nagahama Y.;
"Isolation and characterization of goidfish cdk2, a
of the cell cycle regulator cdc2.";
Dev. Biol. 152:113-120(1992).
-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF TI
INTERACTS WITH CYCLINS A, D, OR E.
-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR
THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACT
SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROCEDCZ/CDKX SUBFAMILY.
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MEDLINE=92331802; PubMed=1339336;
MEDLINE=92431802; PubMed=1349346;
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Science 282:2012-2018(1998).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KI EMBL; AL032618; CAB63367.1; -.
HSSP; P24941; 1HCL.
R WormPep; Y42A5A.4; CE20258.
R InterPro; IPR000719; Prot kinase.
R InterPro; IPR000719; Prot kinase.
R InterPro; IPR00069; pk:nase; 1.
R ProDom; PD000001; Prot kinase; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R ATP-binding; Kinase; Serine/threchine-protein kinase; Tran cfournce 353 AA; 40665 MW; 7E32260D9849CAC9 CRC64;
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O9UZH1;
O1-MAY-2000 (TrEMBLrel. 13, Last sequence updatel-MAR-2003 (TrEMBLrel. 23, Last sequence updatel-MAR-2003 (TrEMBLrel. 23, Last annotation upy Y42A5A.4.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
Steward C.A.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ
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Last sequence up
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A ADMAN M.D. S. S. S. Puble S. A. E. V. Gocayne J.D.,

A ADMAN M.D. S. S. S. Publed 10731132,

A REDILNE-20156006; Publed-10731132,

A REDIL S. S. S. Richards N. A. Mandell M.D. Zhang O. Chemp. L. N.

B REDILOG R. C. Baxer E. G., Helt G., Nelson C., Millog G.L. G.,

B REDILOG R. C. Baxer B. W. Berman B. P. Brandari D., Bolshakov S.,

A BORCHAN, M. AMIRCH M. A. BROUK V. BECKEE'S P., Brottler F.,

A BORCK M. BOOK D. B., BROUK W. BROWEN C. D. WASPERSTORIL L. Beadley E. M.,

A BORCK M. CORP. A., DENG Z., MAYS A.D., Dw. I. Dietz S. M.

Cherry V. M. Cawley S., Danke C., Newsport L. B., Davies P.,

A ROLLY R. C. Busam D. A., Buller H., Caldau E., Center M., Chandra I.,

A ROLLY M. C. Sunger B., Carry M. S., Gelbart M. K.,

A ROLLY M. C. Downes M. Dungel-Scote S., Dw. I. D., Dw. I. Dietz S. M.

B RA GORN K., DOUP L. E. Downes M. Dungel-Scote S., Dw. I. D., Dw. I. D.

A ROLLY M. C. Sunger B., Carry M. S., Carry M. S., Rull D., Lang Y.,

A HARTS N.L., Marrey B., McIncok N. S., Carry M. S., Kill D., Lang Y.,

A HARTS N.L., Marrey B., McIncok N. C., Karaytz S., Kill D., Lang Y.,

A HARTS N.L., Marrey B., McIncok N. C., Worris J., Worshreft A.,

A Markiav G., Milahian N.V., Mobarry C., Morris J., Worshreft A.,

A Markiav G., Milahian N.W., Mobarry C., Morris J., Word S.,

A Markiav G., Milahian N.W., Mobarry C., Morris J., Word S.,

A Markiav G., Milahian S., W., Nixon K., Wuskern D., R.,

A REDIL S. M., Word S., W., Willy M., Sunger M., Stanger N.,

A Markiav G., Siden Klang S., Pan S., Pollard W., Wang S.,

A W. W., Wassarman D.A., Milahian S., W., Woo Q.A.,

A W. W., Wassarman D.A., Worley E., Wang S., Yang S.,

A W. W., Worse E. W., Roundy G., Yang S., Wang S.,

A W. W., Wall M., Worse E. W., Rubin 
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VASCSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFWKGCLK
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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01-FEB-1997 (TrEMBLrel. 02,
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SECUENCE Erain;
Gomi H., Sum W., Finch C.E., Itohara S., Yoshimi K., Thompson R.F.;
Gomi H., Sum W., Finch C.E., Itohara S., Yoshimi K., Thompson R.F.;
"Learning induces a cdc2-related protein kinase, kkiamre.";
"Learning induces a cdc2-related protein kinase.";
"Learning induces a cdc2-related protein kinases.";
"Learning induces a cdc2-related protein kinases.";
"Learning induces a cdc2-related protein kinases.";
"Submitted (UUN-1999) to the EMBL/GenBank/DDBJ databases.
"SEMBL; AB029045; BAA88508.1;
"InterPro; IPR000719; Prot kinase."

InterPro; IPR0002290; Ser thr pkinase.

InterPro; IPR0002290; Ser thr pkinase.

InterPro; IPR0002290; Ser thr pkinase.

InterPro; IPR000220; STKC; I.

SYART; SM0C220; STKC; I.

BROSITE; PS00107; PROTEIN KINASE ATP; I.

PROSITE; PS00108; PROTEIN KINASE ST; I.

RW ATP-binding; Kinase; Seriñe/threonine-protein kinase; Transferase.

SEQUENCE 566 AA; 64052 MW; SD57595550902EA9 CRC64;
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[<u>I</u>
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us.
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SMART; SM00220; S_TKc; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 392 AA; 44962 MW; C9627D077784E55D CRC64;
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e; Oryctolagu:
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,7e-76;
65;
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OPTTKO:

OPTT
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-82;
61;
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ed. No. 8.7e-
Mismatches
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Pred. No. 3.7e
7; Mismatches
                                                                                                                                                 Score
Pred.
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                                                                                                                                               ch
11 Similarity 53.0%;
184; Conservative (
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                                          NCIHRDIKPENILITKOGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG
                                                                                                                                                       1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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Catarrhini; Hominidae; Homo.
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MEDLINE=97152547; Pubmed=9000130;
Taglienti C.A., Wysk M., Davis R.J.;
Taglienti C.A., Wysk M., Davis R.J.;
"Molecular Cloning of the epidermal growth factor-stimular kinase p56 KKIAMRE.";
Oncogene 13:2563-2574(1996).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN I EMBL; U35146; AAC50918.1; -.
HSSP; P24941; 1HCL.
Genew; HGNC:1782; CDKL2.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002209; Ser_thr_pkinase.
Fram; PF00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST: 1.
PROSITE; PS0108; PROTEIN KINASE ST: 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Trais SEQUENCE 493 AA; 56018 MW; 5CC20A91CBF89EFE CRC64;
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                                                                                                                                                                      Score 915.5; DB 4
Pred. No. 6.8e-74;
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NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGJTQYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP
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                EGRNRRRQQ
                             and
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Murinae; Mus
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expression
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OF PROTEIN
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InterPro; IPR000719; Prot kinase.
InterPro; IPR000290; Ser thr pkinase.
Pfam; PF30069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATF; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 568 AA; 64055 MW; A43B75E2E9EB86C4 CRC64;
                 EAQIK--RKARN-
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                    Thompson R.F., dual promoters,
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No. 8.1e-73;
                                                                                                                                           Created)
Last sequence update)
Last annotation update
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=129/SVJ, and C57BL/6;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.I
"The Murine KKIAMRE gene: variants, dual promote: chromosomal localization.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ da: -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF EMBL; AB029073; BAA88439.1; JOINED.
EMBL; AB029070; BAA88439.1; JOINED.
EMBL; AB029070; BAA88439.1; JOINED.
EMBL; AB029072; BAA88439.1; JOINED.
EMBL; AB029072; BAA88439.1; JOINED.
EMBL; AB029072; BAA88439.1; JOINED.
EMBL; AB029072; Cdkl2.

KGD; MGI:1858227; Cdkl2.
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                 CLKMNPDDRLTCSCLLESSYF
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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ilarity 48.6%;
Conservative 6
                                                                                                                                             13,
23,
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Q9QUKO;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
SER/THR kinase KKIAMRE.
CDKL2 OR KKY.
Mus musculus (Mouse).
                                                                                                                  PRELIMINARY
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174; Conserv
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Best Local S
Matches 174
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STRAIN=CSTBL/6; TISSUE=Brain;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
The Murine KKIAMRE gene: variants, dual promoters, expression and chromosomal localization.";
Submitted (CJN-1999) to the EMBL/GenBank/DDBJ databases.

-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; AB029066; BAA88428:1; -.

RSSP; P24941; 1HCL.

RGD; MGI:185827; Cdkl2.

R HSSP; P24941; 1HCL.

RGD; MGI:185827; Cdkl2.

R HSSP; P24941; 1HCL.

RGD; MGI:185827; Cdkl2.

R HSSP; P24941; 1HCL.

R MGD; MGI:185827; Cdkl2.

R MGD; MGI:185827; Cdkl2.

R MGD; MGI:185827; Cdkl2.

R PROOLOG; PROTEIN KINASE ATP; 1.

R PROSITE; PSO011; PROTEIN KINASE DOM; 1.

R PROSITE; PSO011; PROTEIN KINASE DOM; 1.

R PROSITE; PSO011; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 564 AA; 63640 MW; DACDEF630CCE82D5 CRC64;
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                          Euteleostom:
Murinae; Mu
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                                                                                                                                                                                                                                          090Y12
090Y12;
090Y12;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Ser/Thr kinase KKIAMRE-gamma.
CDKL2 OR KKY.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB 11;
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nes 69;
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No. 8.
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48.6%; Pred.
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Matches 174; Conservative
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-!- SIMILARITY: BELONGS TO THE SER/THR FAWILY OF PROTEIN KINASES.

RHSSP; P24941; 1HCL.

RGD; MGI:1858227; Cdk12.

RINterPro; IPR000719; Prot kinase.

RINterPro; IPR002290; Ser thr pkinase.

R InterPro; IPR002290; Ser thr pkinase.

R ProDom; PD000001; Prot kinase.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

RROSITE; PS00107; PROTEIN KINASE DOM; 1.

RROSITE; PS00108; PROTEIN KINASE ST; 1.

RATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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CLHIDPDKRPFCADLLRHJFFQMDGFAERFSQELQLKIEKDARNNSLPKKSQNRK
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                                                                                            090YII)
090YII;
090YII;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ser/Thr kinase KKIAMRE-delta (Fragment).
CDKL2 OR KKM.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M.
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
"The Murine KKIAMRE gene: variants, dual promoters, expression chromosomal localization.";
chromosomal localization.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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SHOW Sapiens (Human).

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

NAMIAME a novel kinase deleted in human leukemia.";

NNIAME a novel kinase deleted in human leukemia.";

REMBL; AF130372; AAF36509:1; -..

Genew, HGNC:15483; CDKL3.

SRART; SM002290; Ser thr_pkinase.

NRART; SM002290; Ser thr_pkinase.

NRART; SM00220; STKC; 1.

NRART; SM00220; STKC; 1.

NRART; SM00220; STKC; 1.

NRART; SM0100; PROTEIN KINASE ATP; 1.

PROSITE; PS00107; PROTEIN KINASE ST; 1.

RECTENCE PS00108; PROTEIN KINASE ST; 1.

RECTENCE 455 AA; 51566 MW; 12046F84A363F7A0 CRC64;
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Catarrhini; Hominidae; Homo.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to cyclin-dependent kinase-like 3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; El Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Formatia; Mominidae; Mo
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on update)
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Best Local Similarity 44.0%; Pred. No. 8.7e-60;
Matches 150; Conservative 61; Mismatches 91;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation
Serine-threonine protein kinase NKIAMRE.
NKIAMRE.
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1. 15,
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PNIVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQAINFCHIH
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Murinae; Mu
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Q8K134;
Q8K134;
Q1-QCT-2C02 (TrEMBLrel. 22, Last sequence update)
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-QCT-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to serine/threonine kinase NKIATRE beta.
CDKL3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mui
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TISSUE=Kidney;
Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ data)
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ data)
EMBL; BCC28871; AAH28871.1; -.
MGD; MGI:2388268; Cdkl3.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Froncm; PF00069; pkinase; 1.
ProDom; PD0C0001; Prot_kinase.
ProDom; PD0C0001; Prot_kinase.
ProDom; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PSC0108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 353 AA; 40619 MW; 7A645EE9FCAE2328 CR
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Pred. No. 1.2e-58;
53; Mismatches 96;
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Best Local Similarity 41.6%;
Matches 149; Conservative 6
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|MDPVERPSCTALMSMAYF
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Sarkar M., Matthews K.;
Sarkar M., Matthews K.;
"Trypanosoma brucei putative MAP kinase.";
Submitted (DEC-2000) to the EMBL/GenBark/DDSJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN HSSP; P24941; 1B38.
InterPro; IPR001092; HLH basic.
InterPro; IPR001092; HLH basic.
InterPro; IPR001092; HLH basic.
InterPro; IPR00109; Frot kinase.
Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
PROSITE; PS00018; HLH 1; I.
PROSITE; PS00109; PROTEIN KINASE DOM; I.
PROSITE; PS00109; PROTEIN KINASE DOM; I.
PROSITE; PS00109; PROTEIN KINASE ST; I.
ATP-binding; Kinase; Serine/threonine-protein kinase; Tra
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OF PRCTEIN
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ database.
EMBL; BC041799; AAH41799.1; -.
Kinase; Cyclin.
SEQUENCE 592 AA; 67513 MW; 281AF08906EB7697 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMNPDDRLTCSQLLESSYF--DSFQE---AQIKRKARNEGR
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Last annotation update
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                                                                                                                                    ore 758.5; DB 4;
ed. No. 1.3e-59;
Mismatches 91;
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Pred.
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                                                                                                                                    Query Match
Best Local Similarity 44.0%;
Matches 150; Conservative 63
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Q9BMG2,
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Putative MAP kinase,
Trypanosoma brucei.
Eukaryota, Euglenozoa, K
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Murinae; Mu
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Sciurognathi; Muridae; Murinae; Mu
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Sciurognathi; Muridae;
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23, Last sequence update)
23, Last annotation update)
NKIATRE alpha homolog.
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OBBL49;
OBBL49;
Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation updat Serine/threonine kinase NKIATRE alpha homolog.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
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STRAIN=C57BL/63; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Ph
"Analysis of the mouse transcriptome based on
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK350990; BAC34488:1; -.
EMBL; AK350990; BAC34488:1; -.
SEQUENCE 457 AA; 51900 MW; 6FCDD36F51152B6
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54; Mismatches
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STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based c
                                                 A
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                                    Q8BKR2
Q8BKR2;
Q8BKR2;
C1-MAR-2003 (TrEMBLrel. 23, Cree 01-MAR-2003 (TrEMBLrel. 23, Last 01-MAR-2003 (TrEMBLrel. 23, Last C1-MAR-2003 (TrEMBLrel. 23, Last Serine/threonine kinase NKIATRE Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; C3 Mammalia; Eutheria; Rodentia; Sc NCBI_TaxID=10090;
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NCBI_TaxID=10090;
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ilarity 42.8%;
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Leishmania mexicana.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINK
EMBL; AJ293284; CAC07960.1; ".

R HSSP; P24941; IB38.

R InterPro; IPR000219; Prot kinase.

R InterPro; IPR002290; Ser thr pkinase.

R ProDom; P5000001; Prot kinase.

R ProDom; P5000001; Prot kinase; 1.

R ProDom; P5001001; Prot kinase; 1.

R PROSITE; PS500107; PROTEIN KINASE ATP; 1.

PROSITE; PS500108; PROTEIN KINASE DOM; 1.

PROSITE; PS500108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transf
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
NCBI_TaxID=5665,
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Q9GRT9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative mitogen-activated protein kinase 6.
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Best Local Similarity 43.7%; Pred. No. 6.8e-58;
Matches 145; Conservative 62; Mismatches 88;
KPVDIWALGCMI: EMATGHPFLPSSSDLDLLHKIVLKV
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STRAIN=MNYC/BZ/62/M379;
Wiese M., Wang Q., Goercke I.;
"Identification of mitogen-activated protein
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Nature 420:563-573(2002).
EMBL; AK046394; BAC32701.1; -.
SEQUENCE 585 AA; 66530 MW; A1867A2A6CDF15A2 CRC64;
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Best Local Similarity 42.5%; Pred. No. 7.9e-58;
Matches 145; Conservative 65; Mismatches 92;
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(NHP) known as human kinase. The human kinases share structural

similarity with animal kinases, more particularly serine or

threonine protein kinases. Human kinase cDNA is useful for the

detection of mutant human kinase for the diagnosis of disease,

and also as a therapeutic. It is useful for screening drugs

offective in the treatment of symptomatic or phenotypic

manifestations perturbing the normal function of NHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

clantification of other cellular gene products related to human

clantification of other cellular gene products related to human

clantification of other cellular gene products related to human

clantification of other cellular gene products related to human

clantification of other cellular gene products related to sevening mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelled NHP probes

are useful for screening human genomic library for identifying

polymorphisms and as primers in amplification assays to detect

mutations within the exons, introns and splice sites that can

be used in diagnostics and pharmacogenomics. Nucleotide construct

encoding NHP products are used to genetically engineer cells

in vivo that functions as bioreactors in the body delivering a

continuous supply of NHP to the body. Nucleotide constructs

encoding functional NHPs are used in gene therapy for the
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                                   English
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The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, lymphoma, melanoma), an immuno disorder (e.g., acquired immunodeficiency, syndrome (AlDS), Addison's disease, altergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis), a growth and developmental disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, infarction), and a lipid disorder (e.g., fatty liver, cholestasis), cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis), cardiovascular disorder (e.g., fatty liver, cholestasis), caucher's disease, Memann-Pick's disease). PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting cetc., among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. PKIN is useful in southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PKIN-10.
cirrhosis; hepatitis; pscriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic; hypotensive; anti-HIV; enzyme.
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Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Bandman O, Nguyen DB, Lu Y, Burford N, Lal P;
MG, Elliott VS, Recipon SA, Kearney L, Lu DAM;
Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J;
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N-PSDB; AAD30557.
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Patterson C,
Tribouley CM,
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Greenwald SR,
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28-JUL-2000;
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(NHP) known as human kinase. The human kinases share structural

similarity with animal kinases, more particularly serine or

threonine protein kinases. Human kinase cDNA is useful for the

derection of mutant human kinase for the diagnosis of disease,

and also as a therapeutic. It is useful for screening drugs

effective in the treatment of symptomatic or phenotypic

manifestations perturbing the normal function of NHP in the

body. The NHP nucleotide sequences are useful for generation of

antibodies, as reagents in diagnostic assays, for the

identification of other cellular gene products related to human

kinases, and as reagents in assays for screening compounds that

are useful for treating mental, biological or medical disorders.

NHP oligonucleotides are used as probes. The labelied NHP probes
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ical disorder.
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polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bicreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the
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                                                                which known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threohine protein kinases, more particularly serine or threohine protein kinases, more particularly serine or threohine protein kinases, human kinase cONA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs of effective in the treatment of symptomatic or phenotyphic manifestations perturbing the normal function of NHP in the body. The NHP mucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labeled MHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression.
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medical
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 biological or
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Pred. No. 1.3e-165;
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315; Conservative
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AAUC3501-AAJ03557 represent novel human protein kinases #1-57. The
novel protein kinases have been identified as members of the tyrosine
or serine/threonine kinase (PTK and STK) families. The polynucleotides
consering protein kinases and the polypeptides may be used in the
prevention, diagnosis and treatment of diseases associated with
inappropriate kinase expression. For example, they may be used to treat
cancers (especially cancers of haematopoietic origin), cardiovascular
disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
immune related diseases (e.g. rheumatoid arthritis), neurological
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. asthma), infectious
disease (e.g. HIV) and reproductive disorders (e.g. infertility).
Additionally, polynucleotides encoding protein kinases may be
used for gene therapy and as DNA probes in diagnostic assays.
The protein kinase polypeptides may be used as antigens in the production
of antibodies against the protein kinases and in assays to identify
modulators of protein kinase expression and activity.
                                                                                                                                                                                                                                           Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
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Pred. No. 8.9e-164;
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Best Local Similarity 93.4%;
Matches 311; Conservative
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(NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human continuates, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying are useful for screening human genomic library for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening compounds useful for treating mental, biological or medical disc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construenceding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoging functional NHPs are used in gene therapy for the
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biological disorder.
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Pred. No. 4.9e-163;
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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies of and kinase antagonists may also be used to down regulate kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, coxidative-stress related disorders, chronic inflammatory bowel disease,
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 multiple sclerosis autoimmunity, diab
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                                       Match 78.0%; Score 1296.5; DB 22; Local Similarity 90.0%; Pred. No. 1.7e-129; es 243; Conservative 19; Mismatches 5; 1
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The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I) (II) and (III) are useful for diagnostic evaluation of disorders.

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and/or cancers. The nucleic acids and neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and striase antagonists may also be used to down regulate kinase antibodies and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, cardiomyopathies, strokes, renal failure, immune disorders, cardiomyopathies, strokes, renal failure, chronic inflammatory belvic disease, multiple sclerosis, asthma, contribis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.
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                                                                                                                                                                                                                                                                                                                           Score 1149; DB 22;
Pred. No. 7.4e-114;
; Mismatches 0;
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                    Sudersanam
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98.6%;
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                   Martinez R,
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AAF44669.
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                                                                                      neurodegenerative
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N-PSDB;
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The invention relates to an isolated 14257 polypeptide and nucleic acid encoding it. The 14257 protein is a protein kinase that acts as a modulating agent in regulating a variety of cellular processes, including cell proliferation, differentiation, growth and division.

The activity of the protein of the invention may be described as; cytostatic; osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive; antiinflammatory; antithyroid; antiatherosclerotic; hypotensive; vasotropic; antiatherosclerotic; phothalmological; immunomodulator and antiarthythmic; virucide; anorectic; metabolic; immunomodulator and analgesic. The protein of the invention may act as a novel diagnostic target or therapeutic agent controlling certain disorders, for example kinase-associated or other 14257-associated disorders. These may include cellular proliferative disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's disease. Other disorders include bone metabolism disorders such as osteoporosis, disorders of the immune system, e.g. inflammatory, diabetes mellitus, osteoarthritis and asthma. Proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphorylation
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/note= "serine/threonine protein kinase
signal site"
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= "tyrosine kinase phosphorylation
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/note= "kinase transferase protein
serine/threonine-protein ATP-binding
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/note= "N-myristoylation
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lar disorder; hypertension;
cell disorder; psoriasis.
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note= "casein
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the invention may also be of use as therapeutic agents in ca disorders such as hypertension and coronary artery disease, endothelial cell disorders, including psoriasis. The current sequence represents a human kinase 14257 amino acid sequence
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                                                            Score 1140; DB 23;
Pred. No. 6e-113;
2; Mismatches 2;
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ilarity 98.2%;
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N-PSDB; ABL07221.
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KKIAMRE kinase, which is isolated from rabbit brain tissue.
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format
                                                 ch 61.8%; Score 1027.5; DB 22; Semilarity 58.4%; Pred. No. 1.4e-100; 184; Conservative 65; Mismatches 61; I
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The sequence data for this patent did not form specification, but was obtained in electronic fat ftp.wipo.int/pub/published_pot_sequences.
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N-PSDB; AAA29745.
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        be used to express recombinant protein for analysis, characterisation therapeutic use, as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gas chromosome markers or tags, to compare endogenous DNA sequences patients to identify potential genetic disorders, as probes to hybrand discover novel related sequences, as a source of PCR primers, an antigen to induce anti-DNA antibodies. The polypeptides can be u in assay to discover biological activity, to raise antibodies, as the markers, and to isolate correlative receptors or ligands. The polynucleotides may also be used for gene therapy for the treatment disorders which are mediated by KKIAMRE kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDDT; human; disease detection and treatment molecule polypeptid anti-inflammatory; immunosuppressive; osteopathic; cytostatic; a haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotrogene therapy; protein replacement therapy; cell proliferative dicancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AI Goodpasture's syndrome; inflammation; osteoporosis; thrombocytop
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larity 54.6%;
Conservative 67
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nes 177; Conser
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29-MAR-2001;
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell clevaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (AIDS), Geodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABU11845, described in the disclosure of the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                            New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis
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s B;
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Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
J, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerst:
David MH, Lewis SA, Chen AJ, Panzer SR, Harris
Sarwaha R, Lo A, Lan RY, Urashka ME;
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Pred. No. 1.5e-92;
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2001US-291280P.
2001US-291849P.
2001US-299428P.
2001US-299776P.
2001US-300001P.
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larity 98.9%;
Conservative
                                                                                                                        GENOMICS INC
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                                                                                                                                                      Jones AL,
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N-PSDB; ABX34679.
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29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
20-JUN-2001;
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                                                                                                                                                                 Human kinase
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                                                                                                                                                                                                                                                                                                                                                                          AB277126 to AB277165 encode the human protein kinases given in ABP96048 to ABP96087. The protein kinases have antiasthmatic, antiinflammatory, antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic, immunosuppressive and vulnerary activities, and can be used in gene therapy. A protein kinase therapeutic agent from the present invention, particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease, migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers (e.g. leukaemias) or wound granulation.
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                                      Human; protein kinase; enzyme; antiasthmatic; antiinflammatory; antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatimmunosuppressive; vulnerary; gene therapy; COPD; asthma; migrai: chronic obstructive pulmonary disease; non-insulin dependent dialerkinson's disease; myocardial infarction; inflammatory bowel dautoimmune disorder; aliograft rejection; graft versus host diseancer; leukaemia; wound granulation.
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a protein kinase, or in gene therapy fo
s disease, migraine, myocardial infarcti
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llarity 58.6%; Pred. No. 4.9e-91;
Conservative 26; Mismatches 59;
                     NO:80
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                    SEQ ID
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                                                                                                                                                                                                                                                                                                         New protein kinase genes a diseases associated with a treating e.g. Parkinson's allograft rejection or can
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                    Human protein kinase
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N-PSDB; ABZ77165.
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                                                                                                                                                                                                                                    DECODE
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07-MAY-2003
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Matches 201;
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The present sequence is novel human protein (NHP) known as human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the disconine protein kinases. Human kinase cDNA is useful for the disconine protein kinases. Human kinase cDNA is useful for the disconine protein kinases. Human kinase cDNA is useful for the disconing dungs and also as a herapeutic. It is useful for screening dungs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the antibodies, as reagents in diagnostic assays, for the construct or identification of other ceilular gene products related to human kinases, and as reagents in assays for screening mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are used in for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression.
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GEIRRERENSQIPKQASDPPALASQHARITGVSHRTQPTLFLK
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Pred. No. 7.9e-76;
0; Mismatches 0;
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                             Protein;
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N-PSDB; AAD03812, AAD03818.
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Search completed: November 13, 2003, 14:18:48 Job time: 37.1631 secs

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NESULT 2
US-09-411-628-4
; Sequence 4, Ap
; Patent No. 642
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Best Local Si
Matches 211;
122
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Sequence ii, Application US/09411628

Sequence ii, Application US/09411628

Sequence ii, Application US/09411628

Sequence ii, Application US/09411628

GENERAL INFORMATION:
APPLICANT: University of Southern California

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

CURRENT FILING DATE: 1999-10-01

EARLIER APPLICATION NUMBER: US 60/102,906

EARLIER FILING DATE: 1998-10-02

NUMBER OF SEC ID NCS: 16

SOFTWARE: FastSEC for Windows Version 4.0

SEQ ID NC II

TENGTH: 358

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-411-628-11
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Pred. No. 2.5e-116;
; Mismatches 41;
US-08-464-517-38

US-08-246-361A-38

US-08-463-772-38

PCT-US93-09945-2

US-08-932-787B-21

US-08-932-787B-21

US-08-932-787B-21

US-08-88B-818C-21

US-09-093-522-22

US-09-093-522-22

US-08-463-090B-9

US-09-093-522-18

US-09-093-522-18

US-09-093-522-18

US-09-093-522-18

US-09-093-522-18

US-08-874-347-21

US-08-874-347-21

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US-08-318-947A-19
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US-08-874-347-25
US-08-874-347-25
Sequence 25, Application US/08874347
Patent No. 5863741
GENERAL INFORMATION:
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE CF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CCRRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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Pred. No. 8.5e-52
); Mismatches 99
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ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELEPHONE: 612-335-5070
TELEPAX: 612-288-9696
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,3
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
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SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acid
TYPE: amino acid
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ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-411-628-10
Sequence 10, Application US/09411628
Fatent No. 6428994
Fatent No. 6428994
Fatent No. 64289994
FILE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
FILE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-01
FARLIER APPLICATION NUMBER: US 60/102,906
FARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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D KINASES
        APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROT
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ 1D NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                  Score 967.5; JB 4;
Pred. No. 2.9e-93;
67; Mismatches 65;
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Fred. No. 1.3e-90;
68; Mismatches 69;
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ORGANISM: Crcytolagus cuniculus
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                                        - PDEVVWPGVT
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Pred. No. 8.5e-52
); Mismatches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,522
FILING DATE: 08-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874,347
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 07039/055002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
                                                                                                                                                                                                     US-09-093-522-25
; Sequence 25, Application US/09093522
; Patent No. 6015700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ellinger, Mark S. REGISTRATION NUMBER: 34,812
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l Similarity 40.0%;
118; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                CCUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OPERATING SYSTEM:
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Best Local S
Matches 118
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PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNP-NGVADGVIKSVLWQTLQA
                                                                                   120 HNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELL
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                                                                                                                                              Score 570; DB 2; I
Pred. No. 8.5e-52;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMANT
                                                                                                                                                                                                                                                                                                                                 CDK2 INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                  Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18,872
ER: 7934-057
                                                                                                                                                                                                                                                US-08-969-106-2

Sequence 2, Application US/08969106

Patent No. 5986055

GENERAL INFORMATION:
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 INTERACT:
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds Lip
STREET: 1155 Avenue of the Americant New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATICN NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-974:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
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ilarity 40.0%;
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COMPUTER: IBM Compatible
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RY: USA
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118; Conser
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COMPUTER READABLE
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MOLECULE TYPE:
8-969-106-2
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                                                      -- PDEVVWPGVT
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and HPS Protein-
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                                                                                                                                 SMPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFF
                                                                                                                SIPE--PEDMETLEEKFSOVHPV----ALNFMKGCLKMNPDDRLTCSQLLESSYF
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                                                                                                                                                                                        Sequence 14, Application US/39266225D; Sequence 14, Application US/39266225D; Patent No. 6573364; Sequence 11, Application US/39266225D; Patent No. 6573364; Sephen; Papplicant: Nandabalan, Krishan; APPLICANT: Kingsmore, Stephen; APPLICANT: Tchernev, Velizar; TILE OF INVENTION: Isolation and Characterization of Her; TILE OF INVENTION: Syndrome (HPS) Protein Complexes and TITLE OF INVENTION: Interacting Proteins; FILE REFERENCE: 15966-523; CURRENT APPLICATION NUMBER: US/09/266,225D; CURRENT FILING DATE: 1999-03-10; NUMBER OF SEQ ID NOS: 19; SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quantitative
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Pred. No. 8.5e-52;
); Mismatches 99;
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; Sequence 113, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quintle OF INVENTION: On a Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.0%; Pr
Matches 118; Conservative 60;
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US-09-266-225D-14
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LENGTH: 298
TYPE: PRT
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 PNIVKLLDVIHTENKLYLVFEFLHQDLKKFMDASALTGIPLFLIKSYLFÇLIQGLAFCHS
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il Similarity 40.0%; Pred. No. 9.5e-52;
118; Conservative 60; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,125
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APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-974:
A6141 PENNIE
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.-09-338-125-2
Sequence 2, Application US/09338125
Parant No. 6521412
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GENERAL INFORMATION:
APPLICANT: Yang, M.
APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 I
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                18;
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                                                                                                                Sequence 13, Application US/09411628

Fatent No. 642894

Fatent No. 642894

Fatent No. 642894

Fatent No. 6428994

Fatent No. 6428994

FILLE OF INVENTION: GENA, GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

CURRENT APPLICATION NUMBER: US 60/102,906

FARLIER FILING DATE: 1999-10-01

EARLIER FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 298

TYPE: PRT

CRADAISM: Homo sapiens
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1.1e-51;
99;
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: 60 South Sixth Street, Suite 3300
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Best Local Similarity 40.0%; Pred. No. 1
Matches 118; Conservative 60; Mismatch
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APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KJ
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-874-347-26
; Sequence 26, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
               SIPE--PEDMETLEEKFSDVHPV-
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(298)
OTHER INFORMATION: Xaa = 09-411-628-13
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                                                                                                         -628-13
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CITY: M
STATE:
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                                                                                                                        Length 544
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99;
                                                                                                                     Match
Local Similarity 40.0%; Pred. No. 2.1e-51;
Les 118; Conservative 60; Mismatches 99;
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l Similarity 40.0%; Pred. No. 2.1e-5
118; Conservative 60; Mismatches
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US-09-417-197-115
US-09-417-197-115
; Sequence 115, Application US/09417197
; Patent No. 6518621
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quarithe OF INVENTION: On A Cellular Response; FILE REFERENCE: 3759-0110F
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 115
; LENGTH: 544
                                                                        ; OTHER INFORMATION: CDK2-EGFP fusion US-09-417-197-113
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                                              Sequence
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US-09-417-197-115
             LENGTH: 544
TYPE: PRT
ORGANISM: Artificial S
FEATURE:
ID NO 113
ENGTH: 544
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Matches
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Query Match
Best Local Similarity
Matches 117; Conser
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US-09-093-522-26
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TOPOLOGY: 1
STATE: MN
COUNTRY: US
ZIP: 55402
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Pred. No. 1.2e-51;
; Mismatches 92;
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                                                                  SOFTWARE: FastSEC for Windows Version 2.
CURRENT AFPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/C55001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Suite
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Patent No. 6315700
GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael F.
TITLE OF INVENTION: CARINII
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 60 South Sixth Street, Su
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                67;
       ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IEM Compatible

OPERATING SYSTEM: DCS

SOFTWARE: FASTSEQ for Wind
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ilarity 37.6%;
Conservative
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TOPOLOGY: linear
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117; Conser
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MOLECULE TYPE:

US-08-874-347-26
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US-09-457-040B-29

; Sequence 29, Application US/09457040B

; Patent No. 6387641

; GENERAL INFORMATION:

; APPLICANT: Vertex Pharmaceuticals Incorporated

; APPLICANT: Vertex Pharmaceuticals Complexes

; TITLE OF INVENTION: Crystallized P38 Complexes

; FILE REFERENCE: VPI/98-14

; CURRENT APPLICATION NUMBER: US/09/457,040B

; CURRENT FILING DATE: 1999-12-08

; NUMBER OF SEQ ID NOS: 41
                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SCETWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,522
FILING DATE: 08-JUN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/874,347
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055062
TELEPHONE: 612-288-9696
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                       : Diskette
IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acid
TYPE: amino acid
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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APPLICANT: Yancopoulos, George D.
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: 2
CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FCRM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FCRM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-CCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING JATE: 03-JAN-1994
CLASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          STAVDIWSLGCIFAEMVTRRALFPGDSEIDQLFRIFRTLGT--
                                                                                                                                                  66
                                                                                                                  Score 567; DB 4;
Pred. No. 1.8e-51;
); Mismatches 99
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SS-08-176-62CA-16

Sequence 16, Application US/08176620A

Patent No. 5595904

GENERAL INFCRMATION:

APPLICANT: Boulton, Teri G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boulton, Teri G.
Cobb, Melanie H.
Yancopoulos, George I.
Nye, Steven
Panayotatos, Nikos
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PENNIE
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                                                                                                                                  11 Similarity 40.0
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Patentin version
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                                                                  ; ORGANISM: Human US-09-457-04CB-29
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TELEX: 6
                SEÇ ID NO 29
LENGTH: 298
TYPE: PRT
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APPLICANT:
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SOFTWARE:
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                                                                    - VWPEVESLQDYKNTFPKWKPGSLASHVKNLDENGLDLLSKMLIYDPAKRISGKMALNHP
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                                                    Gaps
                                                    32;
                                  Length 297;
                                                    Indels
                                                    95;
                                  Score 565; DB 1;
Pred. No. 2.8e-51;
1; Mismatches 99
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                                                    61;
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                                  34.0%;
il Similarity 39.7%;
124; Conservative 61
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unknown
3: protein
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US-08-176-620A-16
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Matches 124
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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- protein search, using sw model OM protein November 13, 2003, 14:16:37 Run on:

/ ; Search time 13.3233 Seconds
(without alignments)
2273.702 Million cell updates/sec

score: Title: Perfect so Sequence:

US-09-671-050-12 1662 1 MEKYEKLAKTGEGSYGVVFK.....RKARNEGRNRRRQQVLPLKS

315

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

prr 76:* 2: pirr:* 3: pir2:* 4: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SULT 1 3383 Otein kina Species: R Date: 15-0 Accession: Meyerson, BC J: 11, Accession: Accession: Status: nu Keywords: nu Keywords: nu 11-19/Regi 34,52,127, Acces Eest Local Katches 2	Cy 121 NCIHRDIKPENILITKQGIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 121 NCIHRDIKPENILITKQGIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 122 NCIHRDVKPENILITKHSVIKLCDFGFARLLTGPSDYYTDYVATRWYRSPELLVGDTQYG CY 180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI 182 PPVDVWAIGCVFAELLSGVPLWPGKSDVDQLYLIRTLGCLIPRHQSIFKSNGFFHGISI ON 240 PEPEDMETLEEKFSDVHPVALNFWKGCLKMNPDDRLTCSOLLESSYFDSFGEAQ 293 240 PEPEDMETLEEKFSDVHPVALNFWKGCLKMNPDDRLTCSOLLESSYFDSFGEAQ 293 241 PDPEDMETLEEKFSDVHPVALNFWKGCLKMNPDDRLTCSOLLESSYFDSFGEAQ 293 242 PDPEDMETLEEKFPNISYPALGLLKGCLHMDPTERLTCEQLLHHPYFENIREIE 295 SETING/Threonine protein kinase KKIALRE (EC 2.7.1) - human C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-199
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MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQ 57	289 FQEACIKRK 29 : : : : : : : : : :	tis, C.E.; week to the EMBL D btion: The unic nce number: S40 ion: S40021 preliminary te type: mRNA es: 1-292 cMIC> references: EMB lis, C.; weeks, Biophys. Acta The isolation	atus: preliminary lecule type: mRNA sidues: 1-18,'Y',20-188,'G',190-292 <mi2> serfamily: kinase-related transforming protein; words: ATP; cell cycle control; phosphoprotein 254/Domain: protein kinase homology <kin> -18/Region: protein kinase ATP-binding motif 51,126,128/Active site: Lys, Glu, Asp, Lys #st ery Match st Local Similarity 37.5%; Pred. No. 1.1e-20 ches 115; Conservative 64; Mismatches 9</kin></mi2></mi2></mi2></mi2></mi2>	1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVK
Meyerson, M.i. Dmitted to the EMBL Data Library, May 1992 Reference number: \$22743 Accession: \$22745 Status: preliminary Molecule type: mRNA Molecule type: mRNA Residues: 1-376 <mey> Cross-references: EMBL:X66359 Genetics: Introns: 152/3: 176/3 Superfamily: kinase-related transforming protein; protein kinase homology Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase 3-296/Domain: protein kinase homology <kin> 11-19/Region: protein kinase ATP-binding motif Cuery Match Anther Similarity 67.6%; Pred: No. 9.5e-49; Matches 211; Conservative 41; Mismatches 41; Indels 19; Gaps</kin></mey>		Oy 162 ATRWYRAPELLVGDTOYGSSVDIWAIGCVFAELLTGOPLWPGKSDVDGLYLIRTLGKLI 221	A STAN TO THE STAN TO THE STAN	Generation of the control of the con

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15,0474
protein kinase (EC 2.7.1.37) cdc2 [similarity] - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 05-May-2000 #sequence_revision 05-May-2000
C;Accession: 156474
R;Kajiura, H.; Yamashita, M.; Katsu, Y.; Nagahama, Y.
Dev. Growth Differ. 35, 647-654, 1993
A;Title: Isolation and characterization of goldfish cdc2, a catalytic composing Reference number: 150474
A;Reference number: 150474
A;Accession: 150474
A;Accession: 150474
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A;Accession: 150474
A;Reference number: Bob EMBL/DDBJ
A;Corss-references: GB:DI7758; NID:g471097; PIDN:BAA04605.1; PID:g471098
C;Superfamily: kinase-related transforming protein; protein kinase homology C;Reywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase ATP-binding motif
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted
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Pred. No. 1.7e-20;
58; Mismatches 90;
                                                                                                                                                                                                                                                                         Score 571.5; DB 2;
Pred. No. 1.5e-20;
7; Mismatches 92;
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-294 <COL>
A;Cross-references: GB:M60526
C;Superfamily: kinase-related transforming protein;
C;Keywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #st
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C; Species: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text C; Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text C; Accession: B40444
R; Colasanti, J.; Tyers, M.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
A; Title: Isolation and characterization of cDNA clones e A; Reference number: A40444; MUID: 91195354; PMID: 2014258
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Pred. No. 1.5e-20;
56; Mismatches 92;
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Local Similarity 37.9%;
tes 118; Conservative 6
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P.Ninomiya-Tsuji, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K. Arithe: Cloring of a human cDNA encoding at a coccarelated kinase by complementation of a file complementation of a human cDNA encoding at a coccarelated kinase by complementation of a file complementation of a coccarelated kinase by complementation of a facescence number A41227, MUID:92020980; PMID:1717994

A; Residues 1-298 - RNNA
A; Residues 1-298 - RNN-114386
A; RNN-114186
A; RN
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A37871
protein kinase (EC 2.7.1.37) cdk2 - African clawed frog
N; Alternate names: cell division control protein CDC2 homolog Egl
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 3C-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 18-J
C; Accession: A37871; S15866; IS1662; S14410
R; Paris, J.; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, Proc. Natl. Acad. Sci. U.S.A. 88, 1039-1043, 1991
A; Title: Cloning by differential screening of a Xenopus cDNA coding
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Pred, No. 2.5e-20
60; Mismatches 93
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C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1*
C;Accession: S22440
R;Hashimoto, J.; Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Suzui
Mol. Gen. Genet. 233, 10-16, 1992
A;Title: Isolation and characterization of cDNA clones encoding cdc2 home
A;Reference number: S22440; MUID:92293101; PMID:1376401
A;Reference number: S22440
A;Accession: S22440
A;Accession: S22440
A;Reference rumber: S22440; MUID:92293101; PMID:1376401
A;Reference rumber: BBL:X60374; NID:920342; PIDN:CAA42922:1; PID:920343
A;Residues: 1-294 cHAS>
A;Cross-references: EMBL:X60374; NID:920342; PIDN:CAA42922:1; PID:920343
C;Superfamily: kinase-related transforming protein; protein kinase homology cKIN>
F;2-256/Domain: protein kinase homology cKIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
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C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992
C;Accession: A41227; S17873; S16520
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N;Alternate names: Egl homolog; protein kinase p34
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Biochem Soc. Trans. 20, 80-84; 1922
A;Titie: Control of cell division in plants.
A;Reference number: A48984; MUID:9233944; PMID:1634002
A;Reference number: A48984; MUID:9233944; PMID:1634002
A;Reference number: A48984; MUID:9233944; PMID:1634002
A;Residues: 1-294 (MIZA)
A;Residues: 1-294 (M
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protein kinase (EC 2.7.1.37) cdc2-A [similarity] - African cl
N;Alternate names: maturation-promoting factor p34cdc2 chain
C;Species: Xenopus laevis (African clawed frog)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_chan
C;Accession: A44349
R;Pickham, K.M.; Meyer, A.N.; Li, J.; Donoghue, D.J.
Mol. Cell. Biol. 12, 3192-3203, 1992
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Matches 111; Conservative 70; Mismatches 93;
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2, PMID:1618302
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protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana
N; Alternate names: cdc2 protein homolog; CDC2a protein; cell divisi
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Bate: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 20.
R; Imajuku, Y.; Hirayama, T.; Endoh, H.; Oka, A.
FEBS Lett. 304, 73-77, 1992
A; Title: Exon-intron organization of the Arabidopsis thaliana proteanition organization organization of the Arabidopsis thaliana proteanition organization organization of the Arabidopsis thaliana proteanition organization organiz
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CY 118 HIHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYIDYVATRWYRAPELLVGDT 176	SULT 14 9271 LL DIVISION CONTROL PROTEIN Alternate names: protein T21 Species: Arabidopsis thalian Date: C2-Jun-2060 #sequence Accession: T49271 Rieger, M.; Gabel, C.; Muell Bmitted to the Protein Seque Reference number: Z25021 Accession: T49271 Status: preliminary Molecule type: DNA Residues: 1-294 <rie> Cross-references: EMBL:AL132 Experimental source: cultiva Genetics: Genetics: Genetics: ATSP:T21J18.20 Map position: 3 Introns: 3/3; 67/3; 105/3; 1 Superfamily: kinase-related Ouery Match Douery Match I MEKYEKLAKTGEGSYG I MEKYEKLAKTGEGSYG I MDOYEKVEKIGEGTYG I MDOYEKVEKIGEGTYG I MDOYEKVEKIGEGTYG I PNLVNLIEVFRREKEN ST.:::</rie>	Cy 120 HNCIHRDIKPENILITKQ-GILKICDFGFAQIL-IPGDAYIDVVATRWYRAPELLVGDTQ 177
A;Title: Requirement of mos(Xe) protein kinase for meiotic maturation of Xenopus occytes A;Reference number: A44349; MJID:92318937; PMID:137775 A;Accession: A44349 A;Molecule type: mRNA A;Residues: 1-3C <pic> A;Residues: 1-3C <pic< 1-3c="" <pic="" a;residues:=""> A;Residues: 1-3C <pic> A;Residues: 1-3C <pic 1-3c="" <pic="" a;residues:=""> A;Residues: 1-3C <pic> A;Residues: 1-3C <pic< td=""><td> MEKYEKLAKIGEGSYGVVFKCANKTSGQVVAVKKFVESEDDPVVKKIALREIRNLKOLKH 60 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1</td><td>cleotide sequences of cDNAs () \$20658 () \$AAN> () \$AAN> () \$1 = MBL:X6C767; NID:957533; () \$2 = EMBL:X6C767; NID:957533; () \$2 = EMBL:X6C767; NID:957533; () \$2 = EMBL:X6C767; NID:95753; () \$2 = EMBL:X6C767; () \$2 = EMBL:X6</td></pic<></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic<></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic></pic>	MEKYEKLAKIGEGSYGVVFKCANKTSGQVVAVKKFVESEDDPVVKKIALREIRNLKOLKH 60 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1	cleotide sequences of cDNAs () \$20658 () \$AAN> () \$AAN> () \$1 = MBL:X6C767; NID:957533; () \$2 = EMBL:X6C767; NID:957533; () \$2 = EMBL:X6C767; NID:957533; () \$2 = EMBL:X6C767; NID:95753; () \$2 = EMBL:X6C767; () \$2 = EMBL:X6

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larity 39.4%; Pred. No. 8.3e-20;
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version :
GenCore (c) 1993
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14:12:56 2003, November 13, Run on:

; ; Search time 9.51662 Seconds (without alignments) 1556.584 Million cell updates/sec

US-09-671-050-12 score: Title: Perfect so Sequence:

1662 1 MEKYEKLAKTGEGSYGVVFK.....RKARNEGRNRRRQQVLPLKS

table:

Scoring

313

127863 seqs, 47026705 residues о . BLOSUM62 Gapop 10.0 , Gapext Scarched:

127863 hits satisfying chosen parameters: οţ number Total

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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R GO; GO:0004693; F:cyclin-dependent protein kinase activity; TAS.
R GO; GO:0000074; P:regulation of cell cycle, TAS.
R GO; GO:000074; P:regulation of cell cycle, TAS.
R DRO00001; PRO0100; Protein kinase.
R PROSITE; PSG00107; PROTEIN KINASE ATP; 1.
R PROSITE; PSG00107; PROTEIN KINASE DOM; 1.
R PROSITE; PSG00107; PROTEIN KINASE DOM; 1.
R PROSITE; PSG00107; PROTEIN KINASE DOM; 1.
R PROSITE; PSG00107; PROTEIN KINASE.
F PROMING 34 ATP (BY SIMILARITY).
F ACT SITE 127 BY SIMILARITY).
SC SEQUENCE 358 AA; 41834 MW; 88344321F24B77C6 CRC64;
                                                                                                                                                                                             Euteleostomi; Homo.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92347325; PubMed=1639063;
MEDLINE=92347325; PubMed=1639063;
Meyerson M., Enders G.H., Wu C.-L., Su L.-K., Gorka C., Nelson C.,
Harlow E., Tsai L.-H.;
"A family of human cdc2-related protein kinases.";
EMBO J. 11:2909-2917(1992).
EMBO J. 11:2909-2917(1992).
-!- SIMILARITY: BELONGS TC THE SER/THR FAMILY OF PROTEIN KINASES.
CDC2/CDKX SUBFAMILY.
                                                                                                                                                                                               Vertebrata; Hominidae
                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase KKIALRE (EC 2.7.
Kinase-like 1).
CDKL1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Primates; Catarrhini; Homini
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PIR; S23383; S23383.
HSSP; P24941; 1HCL.
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Andreesen J.D.;
"Differential screening leads to novel genetic markers of monocyte to macrophage maturation.";
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- CATALYTIC ACTIVITY: ATP + b protein = ADP + a phosphoprotein.
-!- CATALYTIC ACTIVITY: EXPRESSED IN BRAIN, LUNG, KIDNEY, PROSTATE, OVARY, PLACENTA, PANCREAS AND TESTIS.
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, LUNG, KIDNEY, PROSTATE, OVARY, PLACENTA, PANCREAS AND TESTIS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=98389628; PubMed=9721213;
MODLINE=98389628; PubMed=9721213;
MODLINE=98389628; PubMed=9721213;
Montini E., Andolfi G., Caruso A., Buchner G., Walpole S.M.,
Mariani M., Consalez G.G., Trump D., Ballabio A., Franco B.;
Mariani M., Consalez G.G., Trump D., Ballabio A., Franco B.;
"Identification and characterization of a novel serine-threonine
kinase gene from the Xp22 region.";
Genomics 51:427-433(1998).
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CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS
CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE
FRAMESHIFT IN POSITION 415.
                     Score 1183.5; DB 1;
Pred. No. 9.1e-82;
i; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serine/threonine protein kinase 9 (EC 2.7.1.37)
Homo sapiens (Himman)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1030
                                                          41;
                 Match
Local Similarity 71.8%;
es 211; Conservative 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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076039; Q14
15-JUL-1999
15-SEP-2003
                     Query Match
Best Local S
Watches 211
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200526;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cell division protein kinase 3 (EC 2.7.1.-).
CDK3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ion; TAS.
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EMBL; Y15057; CAA75342.1; -..
EMBL; X89059; CAA61445.1; ALT_FRAME.
HSSP; P24941; 1B38.
Genew; HGNC:11411; STK9.
GK; O76039; -..
MIM; 30C203; -..
MIM; 30C203; -..
MIM; 30C203; -..
MIM; 30C203; -..
GO; GO:0004674; F:protein serine/threonine kinase activit
GO; GO:000468; P:protein amino acid phosphorylation; TAS
InterPro; IPR00719; Prot kinase.
InterPro; IPR00719; Prot kinase.
InterPro; IPR00719; Prot kinase.
From Propom; P3000001; Prot kinase; 1.
FROSITE; PS00108; PROTEIN KINASE ATP; 1.
FROSITE; PS00108; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding Phosphorylation.
INTERPROFESTION: ATP (BY SIMILARITY).
FROM BIND
FROM SITE INSTITUTION (ACTIVATES THE PRODE IN ENTRY).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (ACTIVATES
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HR -> GT (IN REF. 2).

L -> W (IN REF. 2).

MISSING (IN REF. 2).

MW; 8AIC9C438610EF08 C
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Pred. No. 1.6e-46;
59; Mismatches 98;
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Best Local Similarity 44.4%;
Matches 139; Conservative
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01-FEB-1999
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                                                                                      PROTEIN KINASES.
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                                       Meyerson M., Enders G.H., Wu C.-L., Su L.-K., Gorke Harlow E., Tsai L.-H.,
"A family of human cdc2-related protein kinases.";
EMBO J. 11:2909-2917(1992).
-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF 'INTERACTS WITH A YET UNKNOWN TYPE OF CYCLIN. C.
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                                                                                      TO THE SER/THR FAMILY
               SEQUENCE FROM N.A.
TISSUE=Fetal brain;
MEDLINE=92347325; PubMed=1639063;
TISSUE=Fetal brain;
MEDLINE=92347325, PubMed=1639063;
TISSUE=Fetal brain;
Primates;
                                                                               HISTONE H1.
SIMILARITY: BELONGS
CDC2/CDKX SUBFAMILY.
Eutheria;
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      NCBI_TaxID=9606
[1]
Mammalia;
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N SEQUENCE FROM N.A.

NEDLINE=94032415; PubMed=8218353;

NA Michaelis C.E., Weeks G.;

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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).
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PIR; S40021; S40021.
EMBL; L00652; AAA16056.1; -.
EMBL; L00652; AAA16056.1; -.
ESSP; P24941; 1CKP.
SictyDb; DD05039; crpA.
InterPrc; IPR00719; Prot_kinase.
InterPrc; IPR002290; Ser_thr_pkinase.
ProDom; PD0000001; Prot_kinase; 1.
ProDom; PD0000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CDC2-like serine/threonine-protein kinase CRP (EC 2 CRPA OR CRP.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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nes 93;
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                            179
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  12
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MEDLINE=93345457; PubMed=8393783;

Poon R.Y.C., Yamashita K., Adamczewski J.P., Hunt T., Shuttleworth J.;

Poon R.Y.C., Yamashita K., Adamczewski J.P., Hunt T., Shuttleworth J.;

"The cdc2-related protein p40MO15 is the catalytic subunit of a protein kinase that can activate p33cdk2 and p34cdc2.";

EMBO J. 12:3123-3132(1993).

-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.

INTERACTS WITH CYCLINS A, D, OR E.

INTERACTS WITH CYCLINS A, D, OR E.

-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
                                                                                                                                                               VAALKE
                                                                               IQSIF-
                                                                                                         KTDFP
                                                                                                                                    SETTES
FCHDH
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DEVELOPMENTAL STAGE: SYNTHESIZED IN UNFERTILIZED EGG, BUT NO LONGER MADE IN THE EARLY EMBRYO.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES CDC2/CDKX SUBFAMILY.
PNIVRLHDVIHTERKLTLVFEYLDQDLKKYLDECGGSISKPTIKSFMYQLLKGVA
                           NCIHRDIKPENILITKOGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVG
                                          --KSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCS
                                                                                                                                                   Vertebrata, Euteleostomi
.a., Pipoidea, Pipidae,
                                                                                 - KLI PRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
TISSUE=Ovary;
MEDLINE=91126051; PubMed=1704128;
Paris J., le Guellec R., Couturier A., le Guellec K., Omilli
Camonis J., Macneill S., Philippe M.;
"Cloning by differential screening of a Xenopus cDNA coding f
protein highly homologous to cdc2.";
Proc. Natl. Acad. Sci. U.S.A. 88:1039-1043(1991).
                                                                                                                                                                                                                                                                                                                                                           homolog
                                                                                                                                                                                                                                                                                                                                                         (CDC2
                                                                               SSVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLG
                                                                                                                                                                                                                                                                                                                  CV-1991 (Rel. 20, Created)

OV-1995 (Rel. 32, Last sequence update)

EB-2003 (Rel. 41, Last annotation update)

division protein kinase 2 (EC 2.7.1.-) (
                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                           LDEK---
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PIR; A37871; A37871.
HSSP; P24941; 18UH.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                              VHPAHQLSSIVHG
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01-NCV-1991
01-NOV-1995
28-FEB-2603
Cell division
kinase).
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"Isolation and characterization of goldfish cdc2, a catalytic component of maturation-promoting factor.";
Dev. Growth Differ. 35:647-654(1993).
-!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYCTIC C CYCLE. IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO S-PHASE MITOSIS. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II. CATALYTIC
Pfam; PF00069; pkinase; 1.

Rrobom; PD000001; Prot_kinase; 1.

RROSITE; PSC0107; PROTEIN_KINASE_ATP; 1.

RROSITE; PSC0108; PROTEIN_KINASE_DOM; 1.

RROSITE; PSC011; PROTEIN_KINASE_DOM; 1.

RROSITE; PSC011; PROTEIN_KINASE_DOM; 1.

R Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; Cell division; Mitosis; Phosphorylation.

T DOWAIN 4 286 ATP (BY SIMILARITY).

T DOWAIN 10 18 ATP (BY SIMILARITY).

T ACT SITE 127 127 BY SIMILARITY).

T MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).

T MOD_RES 150 PHOSPHORYLATION (BY SIMILARITY).

T MOD_RES 160 160 PHOSPHORYLATION (BY SIMILARITY).

T MOD_RES 160 160 PHOSPHORYLATION (BY CRC64;
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Teleostei; Ostariophysi;
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
on control protein 2 homolog (EC 2
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                                                                                                                                                                                                                                                                                                Score 571.5; ; Pred. No. 5.8e-
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P51958;
01-OCT-1996 (Rel. 34, Last sequinocort-1996 (Rel. 40, Last annocell division control protein 2 kinase) (Cyclin-dependent kinase) (Cyclin-dependent kinase) Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Carasinopterygii; Neopterygii; Te Cyprinidae; Carassius.
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38.1%;
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HICEPPO; IPRUC.

R INTERPRO; IPRUC.

R INTERPRO; IPRUC.

R INTERPRO; IPRUC.

R Frodom; Proof kinase; I.

R PROSITE; PSO100; Proof kinase; I.

R PROSITE; PSO3008; PROTEIN KINASE ATP; I.

PROSITE; PSO30108; PROTEIN KINASE ATP; I.

R PROSITE; PSO30108; PROTEIN KINASE DOM; I.

R Transferase; Serine/threonine-protein kinase; ATP-binding;

KW Transferase; Serine/threonine-protein kinase; ATP-binding;

FT DOMAIN

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PROSITE NAME:

FT PROSITE; PSO3010;

ATP BY SIMILARITY).

T SITE 128 BY SIMILARITY).

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T THR-14 OR THR-161 ACT
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R FAMILY OF F
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  PHOSPHORYLATION AT
                      PHOSPHORYLATION AT
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PIR; IS0474; ISC474.
HSSP; C00534; IBI8.
InterPro; IPR060719; Prot_kinase.
InterPro; IPR062290; Ser_thr_pkinase
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                                                              STABLE
                                                                                              SUBCELLULAR LOCATION: N
SIMILARITY: BELONGS TO
CDC2/CDKX SUBFAMILY.
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                                                                                                                                                                                                 variants.";
Mol. Genet. 233:10-16(1992).
-!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC
CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES
THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.
-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATE
THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY
SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CDC2/CDKX SUBFAMILY.
                                                           Tracheophyta
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                                            Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trac)
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae
Ehrhartoideae, Oryzeae, Oryza.
NCBI_TaxID=4530;
                                                                                                                  SEQUENCE FROM N.A.

STRAIN=cv. Nipponbare;

MEDLINE=92293101; PubMed=1376401;

Hashimoto J., Hirabayashi T., Hayano Y., Hata S., Chashi Hashimoto J., Hirabayashi T., Toh-E A., Kikuchi Y.;

Suzuka I., Utsugi T., Toh-E A., Kikuchi Y.;

"Isolation and characterization of cDNA clones encoding chomologues from Oryza sativa: a functional homologue and
  Last sequence update)
Last annotation update)
protein 2 homolog 1 (EC
 update)
01-APR-1993 (Rel. 25, 01-CCT-1996 (Rel. 34, Cell division control
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TISSUE=Ovary;

Yamashita M., Mita K.;

Loun cloning of Cdc2 and cyclin B in medaka species.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBC databases.

CYCLE. IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO S-PHASE AND MITOSIS. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II. CATALYTIC

COMPONENT OF MPF (By similarity).

C -!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATE

SIMILARITY).
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R HSSP; Q00534; 1B18.

R InterPro; IPR000719; Prot_kinase.

R InterPro; IPR00229G; Ser_thr_pkinase.

R InterPro; IPR00229G; Ser_thr_pkinase.

R ProDom; PD000001; Prot_kinase; 1.

R ProDom; PD000001; Prot_kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

R DOMAIN 4 287 PROTEIN KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: FORMS A STABLE BUT NON-COVALENT COMPLEX WITH CYCLIN MATURE COCYTES (By similarity).
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES CDC2/CDKX SUBFAMILY.
                                                                                            protei
AYCHSHRVLHRDLKPQNLLIDRRTNALKLADFGLARAFGIPVRTFTHEVVTLWYR
                          VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSI
                                                                                                                                                                                                                                                                                                                                     Oryzias javanicus (Javanese ricefish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoma Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleoste Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Beloniformes, Adrianichthyidae, Oryziinae, Oryzias.
NCBI_TaxID=123683;
                                                    --TPNEOS
                                                                              --EPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLT
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RYSTPVDVWSTGTIFAELATKKPLFHGDSEIDQLFRIFRTLGTPNNDVWPDVESLPDYKN
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Catarrhini; Hominidae;
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X -> K.
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MEDLINE=91330891; PubMed=1714386;
Elledge S.J., Spottswood M.R.;
"A new human p34 protein kinase, CDK2,
of a cdc28 mutation in Saccharomyces ce
Xenopus Eg1.";
EMBO J. 10:2653-2659(1991).
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MEDLINE=91367262; PubMed=1653904;
Tsai L.-H., Harlow E., Meyerson M.;
"Isolation of the human cdk2 gene that adenovirus ElA-associated p33 kinase.";
Nature 353:174-177(1991).
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MEDLINE=92020980; PubMed=1717994;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cr Mammalia; Eutheria; Primates; Candara; Chordata; Candara; Can
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CDK2_HU
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TISSUE=Placenta;

MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B rownstein M.J., Usdin T.B., Foshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.C., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Schmutz J., Myers R.W.,

B Blakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.;

A Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

F Proc. Nati. Acad. Sci. U.S.A., 99:16899-16933(2022).
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MEDLINE=93010995; PubMed=1396589;
Gu Y., Rosenblatt J., O'Morgan D.O.;
"Cell cycle regulation of CDK2 activity by phosphorylation of and Tyr15.";
EMBO J. 11:3995-4005(1992).
    Matsumoto
                                                                                                                              Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A., Submitted (MAY-2002) to the EMBL/GenBank/DDSJ databases.
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Ninomiya-Tsuji J., Nomoto S., Yasuda H., Reed S.I., Matsum "Cloning of a human cDNA encoding a CDC2-related kinase by complementation of a budding yeast cdc28 mutation."; Proc. Natl. Acad. Sci. U.S.A. 88:9066-9010(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-KAY CRYSTALLCGRAPHY (2.4 ANGSTROMS).
MEDLINE=93288132; PubMed=8510751;
de Bondt H.L., Rosenblatt J., Jancarik J., Jones H.D.,
Morgan D.O., Kim S.-H.;
"Crystal structure of cyclin-dependent kinase 2.";
Nature 363:595-602(1993).
                                                                                                             FROW
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M. NEBLINE-9611126; PubMed-101.

NEBRORA A. JOSEPTO, PubMed-101.
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"Isolation and characterization of cDNA clones er
p34cdc2 homologue from Zea mays.";
Proc. Natl. Acad. Sci. U.S.A. 88:3377-3381(1991).
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                                                                                                                                                                                                                                                                                                                                   Score 567; DB 1
Pred. No. 1.3e-3
; Mismatches
                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                   34.1%;
Jarity 40.0%;
Conservative
10-MAY-01.

27-DEC-00.

09-MAY-01.

17-JAN-01.

14-NOV-01.

06-FEB-02.

06-KUN-C2.

06-KUN-C2.

19-SEP-02.

19-SEP-03.

11-FEB-03.

01-FEB-03.

01-FEB-03.

01-FEB-03.
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118; Conser
1E1X;
1F5Q;
1FVT;
1G11;
1G11;
1G11;
1G11;
1G12;
1H1P;
1H1P;
1H1P;
1H2B;
1H2B;
1H2B;
1H2B;
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Matches 118
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PHOSPHORYLATION (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

PHOSPHORYLATION (BY CAK) (BY SIMILARITY)

S063ECFCC2D5FFDD CRC64;
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      THAT PHOSPHORYLATES
                                                                                                                                                                                           PROTEIN KINASES
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R HSSP; P24941; 1HCL.

R MaizeDB; 60686; -..

R InterPro; IPR00219; Prot kinase.

InterPro; IPR00220; Ser Thr_pkinase.

Promi; P0000001; Prot kinase; I.

Probom; P0000001; Prot kinase; I.

R PROSITE; PS00100; PROTEIN KINASE ATP; I.

PROSITE; PS00100; PROTEIN KINASE DOM; I.

PROSITE; PS0011; PROTEIN KINASE DOM; I.

R PROSITE; PS00101; PROTEIN KINASE.

R PROSITE; PS0011; PROTEIN KINASE.

R PROSITE R PROT
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CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPH
THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.
ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15
THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES
SIMILARITY).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KI
CDC2/CDKX SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Pred. No. 1.4e-35;
56; Mismatches 93;
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ilarity 37.6%;
Conservative 6
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117; Conser
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pubMed=1634002;
P.C.G., Hemerly A.S.,
division in plants.";
ans. 20:80-84(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A. MEDLINE=92339744; Prinze D., Ferreira Pricontrol of cell directions
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SEÇUENCE FROM N.A
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Cricetinae;
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                                                                                                  MEDLINE=21398044; PubMed=11506705;

A Ellenrieder C., Bartosch B., Lee G.Y., Murphy M., Sweeney C., Ellenrieder C., Bartosch B., Lee G.Y., Murphy M., Sweeney C., A Hergersberg M., Carrington M., Jaussi R., Hunt T.;

Hergersberg M., Carrington M., Jaussi R., Hunt T.;

"The long form of CDK2 arises via alternative splicing and form active protein kinase with cyclins A and E.";

DNA Cell Biol. 20:413-423 (2001).

-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYC.

INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAX:

DURING S PHASE AND G2.

-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-160 ACTIVATES IT SIMILARITY).
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                                           Vertebrata; A
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Pred. No. 2.5e-35;
i; Mismatches 99;
                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2
                                                                                                                                                                                                                                              Name=CDK2-alpha;
IsoId=O55076-1; Sequence=Displayed;
Name=CDK2-beta;
IsoId=O55076-2; Sequence=Not described;
SIMILARITY: BELONGS TO THE SER/THR FAMILY
CDC2/CDKX SUBFAMILY.
28-FEB-2003 (Rel. 41, Last annotation update Cell division protein kinase 2 (EC 2.7.1.-). CDK2.
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vert.
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AULLS IACI.
HSSP; P24941; IACI.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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ilarity 39.7%;
Conservative 6
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HSSP; P24941; 1AQ1.
                                                                                                                                                                                                                     SIMILARITY).
ALTERNATIVE PRODUCTS
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117; Conser
                                                              Cricetulus.
NCBI_TaxID=10029;
                                                                                             SEQUENCE FROM N.A
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180
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C P24100; 09M307;
C P24100; 09M307;
T 01-MAR-1992 (Rel. 21, Last sequence update)

T 10-MAR-1992 (Rel. 21, Last annotation update)

T 28-FEB-2003 (Rel. 41, Last annotation update)

T 28-FEB-2003 (Rel. 41, Last annotation update)

CC11 division control protein 2 homolog A (EC 2.7.1.-).

CC12A OR CDC2 OR AT3G48750 OR T21018 20.

CS Arabidopsis thaliana (Mouse-ear cress).

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X REDELINE=21016720; PubMed=11130713;

X Belanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B., Bartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B., Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., & De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P., Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F., & Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S., Wurmbach E., Drzonek H., Holland R., Brandt P., Nyakatura G., Wurmbach E., Drzonek H., Falle H., Holland R., Brandt P., Nyakatura G., Wurmbach E., Schaelo M., Pallavicini A., Toppo S., Simionati B., Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D., RA Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E., Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
                                                                                                                                                               286
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MEDLINE=92316202; PubMed=1618302;
Imajuku Y., Hirayama T., Endoh H., Oka A.;
Exon-intron organization of the Arabidopsis thaliana protein kinase genes CDC2a and CDC2b.";
FEBS Lett. 304:73-77(1992).
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Ferreira P.C.G., Hemerly A.S., Villarroel R., van Montagu M., Inze
"The Arabidopsis functional homolog of the p34cdc2 protein kinase.'
Plant Cell 3:531-540(1991).
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STRAIN=cv. Columbia;
MEDLINE=92039027; PubMed=1937013;
Hirayama T., Imajuku Y., Anai T., Matsui M., Oka A.;
Hirayama T., Imajuku Y., Anai T., Matsui M., Oka A.;
"Identification of two cell-cycle-controlling cdc2 gene homologs
Arabidopsis thaliana.";
Gene 105:159-165(1991).
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Mayer K.F.X., Kaul S., Town C.D., Koc H.D., Tallon L.J., Jenkins J.,
A Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
A Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
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Sasamoto S., Kimura T., Idsamura Y., Sato S., Kato T., Asamizu E.,
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Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
A Watanabe A., Yamada M., Yasuda M., Tabata S.;
T. Sequence and analysis of chromosome 3 of the plant Arabidopsis
T thaliana.";
L. Nature 408:820-822(2000).
CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES
THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.
CHE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.
THE ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
THE ENZYME, WHILE PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CCCCC/CDKX SUBFAMILY.
CHICKLIN: Ref.S sequence differs from that shown due to erroneous
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EMBL; S45387; AAB23443.1; ...

EMBL; S45387; AAB23643.1; ...

EMBL; S45387; CAA4373.1; ...

EMBL; S20895; BAA01623.1; ...

EMBL; S20895; CAA4393.1; ...

EMBL; AS13295; CAA4393.1; ...

EMBL; AS13295; CAA4393.1; ...

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EMBL; AS13295; CAA4393.1; ...

EMBL; AS13296; CAB3996; CAATP, 1.

EMBL; AS13296; CAA4397.1; ...

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TISSUE=Ovary;

Yokota T., Yoshida N., Matsui H., Takahashi T., Yamashita M.;

T "CDNA cloning of medaka (Oryzias latipes) Cdc2.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

CYCLE. IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO S-PHASE AND MITOSIS. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II. CATALYTIC

COMPONENT OF MPF (By similarity).

C -!- ENZYME REGULATION PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY SIMILARITY).
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Q3DGD3;

C38-FEB-2003 (Rel. 41, Created)

C8-FEB-2003 (Rel. 41, Last sequence update)

C61 division control protein 2 homolog (EC 2.7.1.-) (p34 protein 2 hinase) (Cyclin-dependent kinase 1) (CDK1).

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CAchinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostein Achinopterygii; Percomorpha; Atherinomorpha;

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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
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IsoId=Q63699-2; Sequence=Not described;
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
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KEDLINE=96113578; PubMed=8673024;

MEDLINE=96113578; PubMed=8673024;

Hosokawa Y., Yang M., Kaneko S., Tanaka M., Nakashima K.;

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F

"Interaction in rat Nb2 pre-T

"Interaction in ra
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MEDLINE=95166553; PubMed=7862443;
Kotani S., Endo T., Kitagawa M., Higashi H., Onaya T.;
"A variant form of cyclin-dependent kinase 2 (Cdk2) in transformed rat thyroid (FRIL-Tc) cell line.";
Oncogene 10:663-669(1995).
    CRC64
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063699; 009136;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2603 (Rel. 41, Last annotation update)
Ceil division protein kinase 2 (EC 2.7.1.-).
CDK2.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                    Score 561.5; DB 1;
Pred. No. 3.3e-35;
2; Mismatches 92;
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37.5%;
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Best Local Similarit
Marches 116; Conse
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   SEQUENCE
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CDK2_RAT
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9

237

231

180

120

rap.

us-09-671-050-12

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anncunce/or send an email to license@isb-sib.ch).
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REMBL, ABOSO458; BAB17216.1; -.

RICEPPO; IPRO02290; Ser Thr_pkinase.

RICEPPO; IPRO02290; Ser Thr_pkinase.

REMALT, SMC0220; STRC; I.

ROSITE; PSC0107; PROTEIN KINASE ATF; I.

RPOSITE; PSC0108; PROTEIN KINASE DOM; I.

RROSITE; PSC0108; PROTEIN KINASE ST; I.

RROSITE; PROSPHORYLATION (BY SIMILARITY).

ROD_RES IS HOSPHORYLATION (BY SIMILARITY).

RROD_RES IS HOSPHORYLATION (BY SIMILARITY).
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AND
                                                            SEQUENCE FROM N.A.

TISSUE=Ovary;

Yamashita M., Mita K.;

CDNA cloning of Cdc2 and cyclin B in medaka species.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC CELL.

CYCLE. IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO S-PHASE AND MITOSIS. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II. CATALYTIC

COMPONENT OF MPF (By similarity).

-!- SUBUNIT: FORMS A STABLE BUT NON-COVALENT COMPLEX WITH CYCLIN B I MATURE OOCYTES (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

-!- SIMILARITY: BELONGS TO THE SER/THR FAXILY OF PROTEIN KINASES.
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Percomorpha; Ather:
Oryzinae; Oryzias
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Pred. No. 4.7e-35;
71; Mismatches 93;
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Acanthomorpha; Acanthopterygil;
Beloniformes; Adrianichthyidae;
NCBI_TaxID=104658;
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ilarity 37.5%;
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annot-
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK016781; BAC25497.1; -.
EMBL; AK016781; BAC25497.1; -.
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Q8CEQ0;
Q8CEQ0;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
C1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
C1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cyclin-dependent kinase-like 1.
Kus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutexammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
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larity 68.9%; Pred. No. 2.2e-102;
Conservative 42; Mismatches 48;
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                         Q8BLF2
Q8BWI8
Q8IYC7
Q8WXQ5
Q8BVE0
Q9W6R6
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C9vmn3 drosophila
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Science 282:2012-2018(1998).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN FEMBL; AL032618; CAB63367.1; -.
HSSP; P24941; 1HCL.
WormPep; Y42A5A.4; CE2C258.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR000719; Prot_kinase.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
[1]
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InterPro; IPR000719; Prot_kinase.

InterPro; IPR002290; Ser_thr_pkinase.

Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot_kinase; 1.

ProDom; PD000001; Prot_kinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Trist SEQUENCE 493 AA; 56018 MW; 5CC20A91CBF89EFE CRC64;
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MEDLINE=97152547; PubMed=9000130;
Taglienti C.A., Wysk M., Davis R.J.;
"Molecular cloning of the epidermal growth facto kinase p56 KKIAMRE.";
Oncogene 13:2563-2574(1996).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF EMBL; U35146; AAC50918.1; -..
HSSP; P24941; 1HCL.
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larity 53.1%; Pred. No. 6.6e-78;
Conservative 68; Mismatches 69;
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292772;
01-FEB-1997 (TrEMBLrel. 02, CO) 1-FEB-1997 (TrEMBLrel. 02, LO) 1-MAR-2003 (TrEMBLrel. 23, LO) PS6 KKIAMRE protein kinase.
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172; Conser
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C TISSUE=Brain;
Gomi H., Sun W., Finch C.E., Itohara S., Yoshiri K., Thompson R.F.;
Gomi H., Sun W., Finch C.E., Itohara S., Yoshiri K., Thompson R.F.;
"Learning induces a cdc2-related protein kinase, kkiamre.";
"Learning induces a cdc2-related protein kinase, kkiamre.";
"Learning induces a cdc2-related protein kinase, kkiamre.";
"Learning induces a cdc2-related protein kinases."

C -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

BRASD; P24941; 1HCL.

DR HSSP; P24941; 1HCL.

DR PROOF : PROOF Ser thr pkinase.

DR ProDom; PD00000C1; Prot kinase; 1.

DR PROSITE; PS0010; PROTEIN KINASE DCM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

RM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

CONTENT SECOND SERVINE/THREONING-PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

CONTENT SECOND SEC
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e, Cryctolagus
SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DCM; 1.

PROSITE; PS00108; PRCTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase sequence 392 AA; 44962 MW; C9627D077784E55D CRC6
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Pred. No. 3.3e-86;
                                                                                                                            ch 61.8%; Score 1027.5; DB 5, 1 Similarity 58.4%; Pred. No. 6.2e-86; 184; Conservative 65; Mismatches 61;
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1; Leporidae;
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O9TTKO;
O9TTKO;
O1-MAY-2000 (TrEMBLrel. 13, Last
01-MAY-2000 (TrEMBLrel. 13, Last
01-MAR-2003 (TrEMBLrel. 23, Last
ser/Thr kinase KKIAMRE.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Crai
Mammalia; Eutheria; Lagomorpha; Lo
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STRAIN=C57BL/6; TISSUE=Erain;
STRAIN=C57BL/6; TISSUE=Erain;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
"The Murine KKIAMRE gene: variants, dual promoters, expression and chromosomal localization.";
Chromosomal localization.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

REMBL; AB029066; BAA88428.1; -.

ROD; MGI:185827; Cdkl2.

InterPro; IPR00019; Prot kinase.

InterPro; IPR002290; Ser thr pkinase.

REMBL; PS00107; PROTEIN KINASE DOM; 1.

REMBL; PS00107; PROTEIN KINASE ATP; 1.

REMBL; PS00108; PROTEIN KINASE ST; 1.

RATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 564 AA; 63640 MW; DACDEF630CCE82D5 CRC64;
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; Murinae;
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Q9QYI2;
Q9QYI2;
Q9QYI2;
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Ser/Thr kinase KKIAMRE-gamma.
CDKL2 OR KKM.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutemammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus MCBI_TaxID=10090;
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                                                                                             309
                                                                                            --EGRNRRRQQ
                                                                                                       OLKVQKDARNVSLSKKSQNRKKEK
                                                                                             CIK--RKARN--
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st Local Similarity
tches 174; Conser
                                                                                                                                                                                                                                                                         SEQUENCE the STRAIN=C57BL/6; T Sassa T., Gomi H. "The Murine KKIA!" The Murine KKIA!
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Matches
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Murinae, Mu
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expression a
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OF PROTEIN
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=129/SUJ, and C57BL/6;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itoha "The Murine KKIAMRE gene: variants, dual promoters, exprechromosomal localization.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-:-SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL; ABC29063; BAA88439:1; JOINED.
EMBL; ABC29073; BAA88439:1; JOINED.
EMBL; ABC29072; BAA88427:1; -.
RSP; P24941; IHCL.
MGD; MGI:185827; Cdkl2.
InterPro; IPR00719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR002290; Ser thr pkinase.
ProDom; PD000001; Prot kinase; 1.
SMART; SMO0220; Trk; I.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serime/threonine-protein kinase; Tra
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Sciurognathi; Murida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 930.5; DB 11;
Pred. No. 8.2e-77;
66; Mismatches 69;
                                                                                                                                                               Created)
Last sequence update)
Last annotation update
                                                                                                                                568
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EAQIK--RKARN----EGRNRRRQ
| | : | : | | : : : : | | : : : :
ELQLKIEKDARNNSLPKKSQNRKKEK
                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Rodentia
NCBI_TaxID=16090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.0%;
                                                                                                                                                                13
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                                                                                                                             PRELIMINARY
                                                                                                                                                               2000 (TrEMBLrel.
2000 (TrEMBLrel.
2003 (TrEMBLrel.
kinase KKIAMRE.
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RESULT Q9QYI1

Euteleostomi Homc.

KINASES

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MEKYEKLAKTGEGSYGVVFKCRNKTSGOVVAVKKFVESEDDPVVKKJALREJRMLKOLKH
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### SEQUENCE FROM N.A.

### Aidmer M., Haq R., Zanke B.W.;

### Aidmer M., Haq R., Zanke B.W.;

### Scould be an over the state of the st
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Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein Kinase; Sequence 455 AA; 51566 MW; 12046F84A363F7A0 CRC64;
                                                                                                        Vertebrata; ; Hominidae;
    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Serine-threonine protein kinase NKIAMRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 784.5; DB 4;
Pred. No. 1.6e-63;
1; Mismatches 91;
                                                                                                        Craniata; Ve
Catarrhini;
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l Similarity 48.5%; Pre
150; Conservative 61;
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Primates;
                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBIVW4;
01-MAR-2003 (TrEMBLrel. 23, C)
01-MAR-2003 (TrEMBLrel. 23, L,
01-MAR-2003 (TrEMBLrel. 23, L,
5imilar to cyclin-dependent k
Homo sapiens (Human).
Euxaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Strausberg R.;
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NCBI_TaxID=9606
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QBIVW4
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Matches
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OF PROTEIN KINASE.
                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostom
Sciurognathi; Muridae; Murinae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPEDMET--LEEKFSDVHPVALNFMKGCLKMNPDDRITCSQLLESSYF--DSF
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expression
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ProDom; PD00001; Prot_kinase; 1.

SMART; SM00220; S_TKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase;

NON_TER 329 329
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                                                                                                                 090Y11;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ser/Thr kinase KKIAMRE-delta (Fragment).
CDKL2 OR KKM.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                            Thompson R.F., dual promoters,
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F
"The Murine KKIAMRE gene: variants, dual promoter chromosomal localization.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ dat
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF EMBL; AB029067; BAA88429.1; -.
HSSP; P24941; 1HCL.
RGD, MGI:1858227; Cdkl2.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%; Score 928; DB 11;
larity 53.9%; Pred. No. 6.7e-77;
Conservative 63; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F72EB89E65AE8585
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ELQUKI EKDARNNSLPKKSQNRKKEK
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Q9P114;
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                     PRELIMINARY
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173; Conser
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                                                                            PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
                                                                                                                                          SSVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleost; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353;
                                                                                                                                                                                                           286
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                                                                                                                                                                                                                       SVDVEETLQQRFPTAASPWLEFLTSCLRMDPVERPSCTALMSMAYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; 1
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databe BMBL; BC028871; AAH28871.1; -.
MGD; MGI:2388268; Cdkl3.
InterPro; IPR0002290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001290; Ser thr pkinase.
InterPro; IPR001290; Ser thr pkinase.
InterPro; IPR001290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001290; Ser thr pkinase.
InterPro; IPR001290; TyrKc; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
InterPro; IPR001290; Ser thr pkinase.
InterPro; IPR001290; Ser thr pkinase.
IPR051TE; PS00107; PR0TEIN KINASE ST; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
IPR051TE; PS00108; PR0TEIN KINASE ST; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
IPR051TE; PS00108; PR0TEIN KINASE ST; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
IPR051TE; PS00108; PR0TEIN KINASE ST; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
IPR051TE; PS00108; PR0TEIN KINASE ST; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
IPR051TE; PS00108; PR0TEIN KINASE ST; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
IPR051TE; PS00108; PR0TEIN KINASE ST; I.
Reconstruction of the EMBL/GenBank/DDBJ databe
IPR051TE; PS00108; PR0TEIN KINASE ST; I.
                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation updati
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| Similarity 45.7%; Pred. No. 2.4e-62;
| Conservative 63; Mismatches 96;
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Rodentia;
                                                                                                                                                                                                                                                                                                                OBK134
OBK134;
OBK134;
OBK134;
C1-OCT-2002 (TrEMBLrel. 22, C)
01-OCT-2003 (TrEMBLrel. 23, L)
C1-MAR-2003 (TrEMBLrel. 23, L)
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A TISSUE=Kidney;
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Best Local S
Matches 149
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SEQUENCE FROM N.A.

Sarkar M., Matthews K.;

"Trypanosoma bruce; putative Map kinase.";

Submitted (DEC-2000) to the EMBL/GerBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN

EMBL; AF326965; AAG49589.1;

HSSP; P24941; 1B38.

InterPro; IPR001092; HLH basic.

InterPro; IPR000119; Prot kinase.

InterPro; IPR0005290; Ser thr pkinase.

Pfam; PF00069; pkinase; I.

ProDom; PD000001; Prot kinase; I.

ProDom; PD000001; Prot kinase; I.

RMART; SM00220; S.TKC; I.

RROSITE; PS00138; HLH 1; I.

RROSITE; PS00138; HLH 1; I.

RROSITE; PS00107; PROTEIN KINASE DOM; I.

RROSITE; PS00108; PROTEIN KINASE ST; I.

RROSITE; PS00108; PROTEIN KINASE ST; I.

RROSITE; PS00108; PROTEIN KINASE ST; I.

RATP-binding; Kinase; Serine/threonine-protein kinase; Tre

SEQUENCE 657 AA; 72116 MW; C93FA3C2D08F0619 CRC64;
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OF PROTEIN
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                                                                               Length
                                                                                                              Indels
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  database
                                                CRC64;
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81;
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#
                                                                              ore 784.5; DB 4;
ed. No. 2.2e-63;
Mismatches 91;
                                                2B1AF08906EB7697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.0%; Score 781; DB 5; 48.3%; Pred. No. 5.3e-63
EYBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence up
Last annotation
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Q9BMG2;
Q9BMG2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-YAR-2003 (TrEMBLrel. 23, Last annotati
Putative MAP kinase.
Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Tr
NCBI_TaxID=5691;
                                                                               Score
Pred.
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                                                                                                            61;
                                               67513 MW;
                                                                             ch
11 Similarity 48.5%;
150; Conservative 61
Submitted (DEC-2002) to the EMBL; BC041799; AAH41799.1; Kinase; Cyclin. SEQUENCE 592 AA; 67513 XM
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138; Conserv
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Best Local S
Matches 138
                                                                              Query Match
Best Local S
Matches 150
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Euteleostomi; Murinae; Mus

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SSVDIWAIGCVFAELLTGOPLWPGKSDVDOLYLIIRTLGKLIPRHOSIFKSNGFFHGISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK046394; BAC32701.1; -.
SEQUENCE 585 AA; 66530 MW; A1867A2A6CDF15A2 CRC64;
                                                                                                                                                                                                                              Phase I & II
on functional
                                                                                                                                                                                                                                                                                                                                                      CRC64;
                             Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8BL49;
Q8BL49;
C1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Serine/threonine kinase NKIATRE alpha homolog.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                  ore 767.5; DB li;
ed. No. 5.7e-62;
Mismatches 92; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
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46.9%; Pred. No. 1.5e-61;
ive 65; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                        6FCDD36F51152B61
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Verte)
Mammalia; Eutheria; Rodentia; Sciurognathi; M
NCBI_TaxID=1009C;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group P
"Analysis of the mouse transcriptome based on 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK050990; BAC34488.1; -.
SEQUENCE 457 AA; 51900 MW; 6FCDD36F511528
                                                                                                                                                                                                                                 Group
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Genome Exploration Resear
                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
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ilarity 47.2%;
Conservative 64
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145; Conservative
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Best Local Simi
Matches 146;
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Best Local S
Matches 145
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Leishmania mexicana.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
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ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; T; SEQUENCE 1106 AA; 118884 MW; 24AC26F5C209923E CRC64
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Q8BKR2;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Serine/threonine kinase NKIATRE alpha homolog.
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mitogen-activated protein kinase 6.
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Pred. No. 1.2e-61;
2; Mismatches 88;
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InterPro; IPR000719; Prot kinase.
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Pfam; PFC0069; pkinase; 1.
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ò	61 PNIVNLIEVPRRKRKMHIVFEYCDHTLINELERNPNGVADGVIKSVLWQTLCAINFCHIH 120
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ò	121 NCIHRDIKPENILITKOGIIKICDEGEAOIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
QQ	120 NIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDVYTDYVATRWYRAPELVLKDTSYG 179
ò	180 SSVDIWAIGCVFAELLTGOPLWPGKSDVDOLYLIRTLGKLIPRHQSIFKSNGFFHGISI 239
DÞ	180 KPVDIWALGCMITEMATGHPFLPSSSDLDLLHKIVLKVGNLTPHLHNIFSKSPIFAGVVL 239
ò	240 PEPEDMETLEEKFSDVHPVALNFWKGCLKMNPDDRLTCSQLLESSYFDSFQEAQI 294
qq	240 PQVQHPKTARKKYPKLNGLLADIVHACLQIDPAERTSSTDLLRHDYFTRDGFIEKFIFEL 299
ò	295 KRKARNEGR 303
qg	300 RAKLLQEAK 308

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